

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model
Run on: March 5, 2006, 10:17:20 ; Search time 824 Seconds
(without alignments)
8259.342 Million cell updates/sec

Title: US-10-660-208-90
Perfect score: 823
Sequence: 1 ctgacggtagctccaagtat.....cgatccattctccagcgag 823

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:
1: /cgn2_6/ptodata/1/pubna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubna/US08_PUBCOMB.seq.*
3: /cgn2_6/ptodata/1/pubna/US09A_PUBCOMB.seq.*
4: /cgn2_6/ptodata/1/pubna/US09B_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubna/US10A_PUBCOMB.seq.*
6: /cgn2_6/ptodata/1/pubna/US10B_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubna/US10C_PUBCOMB.seq.*
8: /cgn2_6/ptodata/1/pubna/US10D_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubna/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	823	100.0	823	3	US-09-846-903-90
2	823	100.0	823	7	US-10-660-208-90
3	564	68.5	1587	3	US-09-846-903-87
4	564	68.5	1587	7	US-10-660-208-87
5	231	28.1	1578	7	US-10-425-114-22826
6	229	27.8	651	8	US-10-425-115-18768
7	220.2	26.8	1326	7	US-10-425-114-31817
8	220.2	26.8	2760	8	US-10-425-115-69837
9	209.2	25.4	6550	7	US-10-759-602-1
10	209.2	25.4	9299	7	US-10-759-602-15
11	209.2	25.4	9408	7	US-10-759-602-16
12	179.6	21.8	814	8	US-10-425-115-134827
13	179.4	21.8	485	7	US-10-425-114-23949
14	177.8	21.6	379	8	US-10-425-115-34629
15	143.2	17.4	443	8	US-10-425-115-57384
16	127.4	15.5	1014	8	US-10-425-115-145839
17	123.2	15.0	1088	8	US-10-739-930-2967
18	123	14.9	812	8	US-10-425-115-74208
19	113.4	13.8	802	8	US-10-425-115-36797
20	110.2	13.4	720	3	US-09-950-933A-8
21	99.4	12.1	460	8	US-10-425-115-60268
22	99.2	12.1	737	7	US-10-425-114-27876
23	84.6	10.3	521	8	US-10-425-115-24447

ALIGNMENTS

RESULT 1
US-09-846-903-90
; Sequence 90, Application US/09846903
; Publication No. US20030200565A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Dubois, Patrice
; APPLICANT: Malven, Marianne
; APPLICANT: Masucci, James D.
; TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL
; TITLE OF INVENTION: OF GENE EXPRESSION
; FILE REFERENCE: 38-21(15678)B promoters
; CURRENT APPLICATION NUMBER: US/09/846,903
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/201,255
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 90
; LENGTH: 823
; TYPE: DNA
; ORGANISM: Zea mays
US-09-846-903-90

Query Match	100.0%	Score 823	DB 3	Length 823
Best Local Similarity	100.0%	Pred. No. 1.5e+239	Indels 0	Gaps 0
Matches 823	Conservative 0	Mismatches 0		
Qy	1	CTGACCGGTACTCTCAAGTATAAGACACAGCTAAACACACATTAATGCGTGGTCAATGC 60		
Db	1	CTGACCGGTACTCTCAAGTATAAGACACAGCTAAACACACATTAATGCGTGGTCAATGC 60		
Qy	61	TAAACATGTCCTTACCATTTTATCAATCAATCAAGACATTCATTAATTAAGTGA 120		
Db	61	TAAACATGTCCTTACCATTTTATCAATCAATCAAGACATTCATTAATTAAGTGA 120		
Qy	121	CCATCAAGTAGTCTCTGTCGCGAATATAGAGCTTAAGACACTGTCTTCTCGTCAAGATA 180		
Db	121	CCATCAAGTAGTCTCTGTCGCGAATATAGAGCTTAAGACACTGTCTTCTCGTCAAGATA 180		
Qy	181	CATGCTTTGAGATTTTATACATTCACCCCTAGACACACTCTTAAGACACAACTTAAGAC 240		
Db	181	CATGCTTTGAGATTTTATACATTCACCCCTAGACACACTCTTAAGACACAACTTAAGAC 240		
Qy	241	ACCATTTGATACGTCCTTAACCTGACACCGGTACTAGGGCTATTCAAGAACCAACCATG 300		
Db	241	ACCATTTGATACGTCCTTAACCTGACACCGGTACTAGGGCTATTCAAGAACCAACCATG 300		

241 ACCATTGTACATGCCCTAACTGGCACCGCTAGCTAGGGCTATTCAAGAACCAACCATG 300
301 TACAGTTGTGCAACGCTGAATGGTTATTGCTTCAGATTAAAGCTAATATTAGACTGA 360
301 TACAGTTGTGCAACGCTGAATGGTTATTGCTTCAGATTAAAGCTAATATTAGACTGA 360
361 TGCAGCTCAATTCATAGAGCAAAAACAGTGTAGAACCGGTATAGCAATTAAGCAACA 420
361 TGCAGCTCAATTCATAGAGCAAAAACAGTGTAGAACCGGTATAGCAATTAAGCAACA 420
421 AGCGAACAATTCATAGCTTACAACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
421 AGCGAACAATTCATAGCTTACAACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
481 GTGGCTGATATTGCTGAAATTAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
481 GTGGCTGATATTGCTGAAATTAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
541 CAGCAATTCGTTGTTGTTAAAGCTCTCGATTAATTTGTTCACTTAAATAGACCAAGTTCAA 600
541 CAGCAATTCGTTGTTGTTAAAGCTCTCGATTAATTTGTTCACTTAAATAGACCAAGTTCAA 600
601 TTCTGGTTCTAGTCAACATGCTGATCCAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
601 TTCTGGTTCTAGTCAACATGCTGATCCAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
661 GCCGAGTGAGGCCAAGCGGAGCGCGTCCGTCGCTCAACACACCCCTCGTTTACTAT 720
661 GCCGAGTGAGGCCAAGCGGAGCGCGTCCGTCGCTCAACACACCCCTCGTTTACTAT 720
721 ATATACACAGAGCGACGATACCCATATCGTGTGCTAGAGCACTGAAACAGCCGAGC 780
721 ATATACACAGAGCGACGATACCCATATCGTGTGCTAGAGCACTGAAACAGCCGAGC 780
781 GATCTCTCTCCCTCTCCCTCTCCGATCCATTTCTCCAGCGAG 823
781 GATCTCTCTCCCTCTCCCTCTCCGATCCATTTCTCCAGCGAG 823

RESULT 2
US-10-660-208-90
; Sequence 90, Application US/10660208
; Publication No. US20040133946A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Dubois, Patrice
; APPLICANT: Malven, Marianne
; APPLICANT: Masucci, James D.
; TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL
; FILE REFERENCE: 38-21(15678)B promoters
; CURRENT APPLICATION NUMBER: US/10/660,208
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 60/201,255
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 90
; LENGTH: 823
; TYPE: DNA
; ORGANISM: Zea mays

US-10-660-208-90

Query Match 100.0%; Score 823; DB 7; Length 823;
Best Local Similarity 100.0%; Pred. No. 1.5e-239;
Matches 823; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CTGCAAGTACTCCAGTATAGACACACTTAAACACACATATGCGAGTGGTCAATGC 60
1 CTGCAAGTACTCCAGTATAGACACACTTAAACACACATATGCGAGTGGTCAATGC 60
61 TAAACATGTCTTACCATATTCTGTTATCAATCAGAACATTTCAATAAATTAAGTGA 120

61 TAAACATGTCTTACCATATTCTGTTATCAATCAGAACATTTCAATAAATTAAGTGA 120
121 CCATCAGATAGTCTCTCTGTCCTGATATAGAGCTAGAGCACTGTGTCTTCTCGTCAAGATA 180
121 CCATCAGATAGTCTCTCTGTCCTGATATAGAGCTAGAGCACTGTGTCTTCTCGTCAAGATA 180
181 CATGCTCTGAGATTTTTCATTTACATTTACCCCCCTAGACACACTCTTAAGACACAACCTTAAGAC 240
181 CATGCTCTGAGATTTTTCATTTACATTTACCCCCCTAGACACACTCTTAAGACACAACCTTAAGAC 240
241 ACCATTTGATACATGCTTAACTGACACCGCTAGTAGGGCTATTCAAGAACCAACCATG 300
241 ACCATTTGATACATGCTTAACTGACACCGCTAGTAGGGCTATTCAAGAACCAACCATG 300
301 TACAGTTGTTGCAACGTTGAATGTTATTTCTCTCAGATTAAAGCTAATTTTAGACTGA 360
301 TACAGTTGTTGCAACGTTGAATGTTATTTCTCTCAGATTAAAGCTAATTTTAGACTGA 360
361 TGCAGCTGCAATTCATAGAGCAAAAACAGTGTAGAACCGGTATAGCAATTAAGCAACA 420
361 TGCAGCTGCAATTCATAGAGCAAAAACAGTGTAGAACCGGTATAGCAATTAAGCAACA 420
421 AGCGAACAATTCGTTAGCTCAACCAATTTGCTGGGCTTCCATGGGCTCGCAGAGTATT 480
421 AGCGAACAATTCGTTAGCTCAACCAATTTGCTGGGCTTCCATGGGCTCGCAGAGTATT 480
481 GTGGCTGATATTGCTGAAATTAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
481 GTGGCTGATATTGCTGAAATTAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
541 CAGCAATTCGTTGTTGTTAAAGCTCTCGATTAATTTGTTCACTTAAATAGACCAAGTTCAA 600
541 CAGCAATTCGTTGTTGTTAAAGCTCTCGATTAATTTGTTCACTTAAATAGACCAAGTTCAA 600
601 TTCTGGTTCTAGTCAACATGCTGATCCAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
601 TTCTGGTTCTAGTCAACATGCTGATCCAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
661 GCCGAGTGAGGCCAAGCGGAGCGCGTCCGTCGCTCAACACACCCCTCGTTTACTAT 720
661 GCCGAGTGAGGCCAAGCGGAGCGCGTCCGTCGCTCAACACACCCCTCGTTTACTAT 720
721 ATATACACAGAGCGACGATACCCATATCGTGTGCTAGAGCACTGAAACAGCCGAGC 780
721 ATATACACAGAGCGACGATACCCATATCGTGTGCTAGAGCACTGAAACAGCCGAGC 780
781 GATCTCTCTCCCTCTCCCTCTCCGATCCATTTCTCCAGCGAG 823
781 GATCTCTCTCCCTCTCCCTCTCCGATCCATTTCTCCAGCGAG 823

RESULT 3
US-09-846-903-87
; Sequence 87, Application US/09846903
; Publication No. US20030200565A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Dubois, Patrice
; APPLICANT: Malven, Marianne
; APPLICANT: Masucci, James D.
; TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL
; FILE REFERENCE: 38-21(15678)B promoters
; CURRENT APPLICATION NUMBER: US/09/846,903
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/201,255
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 87
; LENGTH: 1587
; TYPE: DNA
; ORGANISM: Zea mays

US-09-846-903-87

Query Match 68.5%; Score 564; DB 3; Length 1587;
Best Local Similarity 99.1%; Pred. No. 1.8e-160;
Matches 567; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 252 ATGCCCTAACTGGCAGCGCTACGTAGGGGCTATTCAAGAACCAACCAATGTACAGTTGTTG 311
DB 992 ATGGCTTAACTGGCAGCGCTACGTAGGGGCTATTCAAGAACCAACCAATGTACAGTTGTTG 1051
QY 312 CAACGTGAATGGTTATTGCTTCCAGATTAAAGCTAAATTTATTAGACTGATGCGAGTCAAA 371
DB 1052 CAACGTGAATGGTTATTGCTTCCAGATTAAAGCTAAATTTATTAGACTGATGCGAGTCAAA 1111
QY 372 TTCATAGAGACAAAACAGTGTAGAGCCGTATAAGCATTTAAGCAAAACAGCGAACATTG 431
DB 1112 TTCATAGAGACAAAACAGTGTAGAGCCGTATAAGCATTTAAGCAAAACAGCGAACATTG 1171
QY 432 CTTAGCTACAACTATTGCTGGGCTTCCATGGGCATCGCAGAAAGTATTGTGGCTGCATA 491
DB 1172 CTTAGCTACAACTATTGCTGGGCTTCCATGGGCATCGCAGAAAGTATTGTGGCTGCATA 1231
QY 492 TTGCTGAAATTTATAGCAGGCGCCCAAGGCCCATCACTTTCAGAGTTCAGCAATTTGTAC 551
DB 1232 TTGCTGAAATTTATAGCAGGCGCCCAAGGCCCATCACTTTCAGAGTTCAGCAATTTGTAC 1291
QY 552 TTTTGTAACTGCTCGATTAATTTGTTCACTTAAATAGACCAATTCATTTCTGTTCTA 611
DB 1292 TTTTGTAACTGCTCGATTAATTTGTTCACTTAAATAGACCAATTCATTTCTGTTCTA 1351
QY 612 GTCAACATGCTCGATTAATTTGTTCACTTAAATAGACCAATTCATTTCTGTTCTA 671
DB 1352 GTCAACATGCTCGATTAATTTGTTCACTTAAATAGACCAATTCATTTCTGTTCTA 1411
QY 672 GCCAAGCGAGCGCGTGTGCTGAGGAGCGAGGAGCGAATGTGGCCCGCGCAGTGAG 731
DB 1412 GCCAAGCGAGCGCGTGTGCTGAGGAGCGAGGAGCGAATGTGGCCCGCGCAGTGAG 1471
QY 732 CGCAGATACCCATATCGTGTGCTGAGGAGCGAGGAGCGAATGTGGCCCGCGCAGTGAG 791
DB 1472 CGCAGATACCCATATCGTGTGCTGAGGAGCGAGGAGCGAATGTGGCCCGCGCAGTGAG 1531
QY 792 CCTCTCCCTCTCCGATCCATTTCCAGCGCAG 823
DB 1532 CCTCTCCCTCTCCGATCCATTTCCAGCGCAG 1563

RESULT 4

US-10-660-208-87
; Sequence 87, Application US/10660208
; Publication No. US20040133948A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Dubois, Patrice
; APPLICANT: Malven, Marianne
; APPLICANT: Maucucci, James D.
; TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL
; FILE REFERENCE: 38-21(15678)B promoters
; CURRENT FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 60/201,255
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
; LENGTH: 1587
; TYPE: DNA
; ORGANISM: Zea mays
Query Match 68.5%; Score 564; DB 7; Length 1587;
Best Local Similarity 99.1%; Pred. No. 1.8e-160;

Matches 567; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 252 ATGCCCTAACTGGCAGCGCTACGTAGGGGCTATTCAAGAACCAACCAATGTACAGTTGTTG 311
DB 992 ATGGCTTAACTGGCAGCGCTACGTAGGGGCTATTCAAGAACCAACCAATGTACAGTTGTTG 1051
QY 312 CAACGTGAATGGTTATTGCTTCCAGATTAAAGCTAAATTTATTAGACTGATGCGAGTCAAA 371
DB 1052 CAACGTGAATGGTTATTGCTTCCAGATTAAAGCTAAATTTATTAGACTGATGCGAGTCAAA 1111
QY 372 TTCATAGAGACAAAACAGTGTAGAGCCGTATAAGCATTTAAGCAAAACAGCGAACATTG 431
DB 1112 TTCATAGAGACAAAACAGTGTAGAGCCGTATAAGCATTTAAGCAAAACAGCGAACATTG 1171
QY 432 CTTAGCTACAACTATTGCTGGGCTTCCATGGGCATCGCAGAAAGTATTGTGGCTGCATA 491
DB 1172 CTTAGCTACAACTATTGCTGGGCTTCCATGGGCATCGCAGAAAGTATTGTGGCTGCATA 1231
QY 492 TTGCTGAAATTTATAGCAGGCGCCCAAGGCCCATCACTTTCAGAGTTCAGCAATTTGTAC 551
DB 1232 TTGCTGAAATTTATAGCAGGCGCCCAAGGCCCATCACTTTCAGAGTTCAGCAATTTGTAC 1291
QY 552 TTTTGTAACTGCTCGATTAATTTGTTCACTTAAATAGACCAATTCATTTCTGTTCTA 611
DB 1292 TTTTGTAACTGCTCGATTAATTTGTTCACTTAAATAGACCAATTCATTTCTGTTCTA 1351
QY 612 GTCAACATGCTCGATTAATTTGTTCACTTAAATAGACCAATTCATTTCTGTTCTA 671
DB 1352 GTCAACATGCTCGATTAATTTGTTCACTTAAATAGACCAATTCATTTCTGTTCTA 1411
QY 672 GCCAAGCGAGCGCGTGTGCTGAGGAGCGAGGAGCGAATGTGGCCCGCGCAGTGAG 731
DB 1412 GCCAAGCGAGCGCGTGTGCTGAGGAGCGAGGAGCGAATGTGGCCCGCGCAGTGAG 1471
QY 732 CGCAGATACCCATATCGTGTGCTGAGGAGCGAGGAGCGAATGTGGCCCGCGCAGTGAG 791
DB 1472 CGCAGATACCCATATCGTGTGCTGAGGAGCGAGGAGCGAATGTGGCCCGCGCAGTGAG 1531
QY 792 CCTCTCCCTCTCCGATCCATTTCCAGCGCAG 823
DB 1532 CCTCTCCCTCTCCGATCCATTTCCAGCGCAG 1563

RESULT 5

US-10-425-114-22826/c
; Sequence 22826, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 22826
; LENGTH: 1578
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3591-120-All_FLI
US-10-425-114-22826

Query Match 28.1%; Score 231; DB 7; Length 1578;

Best Local Similarity 92.4%; Pred. No. 5.2e-59;

Matches 243; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 2 TGCACGGTACTCCAGTATAAGACACAGCTAAACACAACTAATGCGTGGTCTCTCT 61

1054	Db	 TGCACGGTACTCAAGTATAGACACACTAAACACCAATATACTACGTGGACGTGCT	995
62	Qy	 AAACAATGTGCTCTTACCATTATTCATTGTATCAATCAGAACATTTCAATAAATTAAGTGAC	121
994	Db	 AAACAATGTGCTCTTACCATTATTAATTTGTACCAATCAGAGCAATTTCAATAAATTAAGTGAC	935
122	Qy	 CAATCAGATAGTCTCTGTGCCGAATATAGAGCTTAAGACACTGTGCTTCCTCGTCAAGATAC	181
934	Db	 CAATCAGCTAGTCTCATGTCTCGAACATAGAGCTTAAGACACTGTGCTTCCTCGTCAAGATAC	875
182	Qy	 ATGCTTTGGATTTTTTACATCTACCCCTTAGACACACTCTTAGACACAACTTAGACA	241
874	Db	 ATATCTTTGAGTTTTTTTTACATTCACCCCCCTAAACACACTCGAAGACATTAACCTCAAGACA	815
242	Qy	 CCCATGTACATGCCCTAACTGG	264
814	Db	 CCCACTGTACATGCCCTAATCGG	792

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RESULT 6
US-10-425-115-18768
; Sequence 18768, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 18768
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_117117C.1
US-10-425-115-18768

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Query Match	27.8%	Score	229	DB	8	Length	651
Best Local Similarity	92.3%	Prod. No.	1.3e-58				
Matches	241	Conservative	0	Mismatches	28	Indels	0
						Gaps	0
Qy	1	CTGCACGGTACTCTCAAGATATAAGACACAGCTAAAAACAACAATATGCAGTGGTCAATGC	60				
Db	211	CTGCACGGTAGTCTCTAAGTATAAGACACAACTAAAAACAATATAATACAGTGGTCAATGC	270				
Qy	61	TAAACATGTGTCCTTACCATATTCATTTGTATCAATCGAAACATCAATAAATTAAGTGA	120				
Db	271	TAAATATGTGTCCTTACCATATTCATTTGTACCAATCAAGACATTCATAAATTAAGTGA	330				
Qy	121	CCAATCAGATAGTCTCTGTGCCGAATATAGAGCTTAAGACACTGTGTCTTCGTCAAGATA	180				
Db	331	TCAATCAGCTAGTCTTCTCTCTCGAAACATAGAGCTTAAGATACTGTGTCTTTGTCAAGATA	390				
Qy	181	CATGTCCTTGACATTTTTTACATTCACCCCTCTAGACACACTCTTAGACACACAACCTTAAGAC	240				
Db	391	CATGCTTGTAGTTTTTTTTTACATTCACCCCTCTTAGACACACTCTTAAGACACAACCTTAAGAC	450				
Qy	241	ACCCATTGTACATGCCCTTAAC	261				
Db	451	ACCCATTGTACATGCCCTTAC	471				

RESULT 7
US-10-425-114-31817
; Sequence 31817, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:

```

; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 31817
; LENGTH: 1326
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73222F10_FLI
; US-10-425-114-31817

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Query Match	26.8%; Score 220.2; DB 7; Length 1326;
Best Local Similarity	91.1%; Pred. No. 9.1e-56;
Matches 245; Conservative	0; Mismatches 23; Indels 1; Gaps ^a 1;
Qy	1 CTGCACGGTACTCCAAAGTATAAGACACAGCTAAAACACAACAATAATGCAGTGGTGTCATGTC 60
Dd	134 CTGCACGGTACTATAAGTATAAGACACACAATAAACAACAACATGAATGCGTGCATGTC 193
Qy	61 TAAAACATGTGCTTTACCATTATTCATTGTATCAATCAGAACATTCATTAATTAAGAATGA 120
Dd	194 TAAAACATGTGCTTTACCATTATTCATTCAACCAATCAGAGCATTCATTAATTAAGAATGA 253
Qy	121 CCAATCAGATAGTGTCTCTGTGCCGAATATAGAGCTTAAGACACTGTGCTTTGCTCAAGATA 180
Dd	254 CCTATCAGCTAGTGTCTCTGTCTCCAATAGAGCTTAAGACATTGTGCTTCGTCAAGATA 313
Qy	181 CATGCTCTTGAGATTTTTTACATTCACCCCCTAGACACACTCTTAAGACACAACTTTAAGAC 240
Dd	314 CATGCTCTTGAGTTTTTTTTTACATTCACCCCTTAGACACTTTTAAGACACAACTTTAAGAC 372
Qy	241 ACCATTGTACATGCCCTTAACCTGGCACCG 269
Dd	373 ACATATTGTACATGCCCTTAAGGGGAGTCG 401

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RESULT 8
US-10-425-115-69837/c
; Sequence 69837, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 69837
; LENGTH: 2760
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_163683C.1
US-10-425-115-69837

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Query Match 26.8%; Score 220.2; DB 8; Length 2760;
Best Local Similarity 91.1%; Pred. No. 1.4e-55;
Matches 245; Conservative 0; Mismatches 23; Indels 1; Gaps 0

Db 1522 GACCAATCAGTAGCTCTCTGTCGAACATAGAGCTAAGACATTGTGTCTCGTCAAGA 1581
Qy 179 TACATGCTTGTAGATTTTACATTCACCCCTAGACACACTCTAAGACACAACCTTAAG 238
Db 1582 TACATGCTTGTAGATTTTATATATTCACCTCCCAAGACACACTCTAAGACACAACGTAAC 1641
Qy 239 ACACCCATTGTACATGCCCTAA 260
Db 1642 ACACCCATTGTACATGCTCTTA 1663

RESULT 11

US-10-759-602-16

; Sequence 16, Application US/10759602

; Publication No. US20040143868A1

; GENERAL INFORMATION:

; APPLICANT: Armstong, Katherine

; Belmat, Scott

; Folkerts, Otto

; Hopkins, Nicole

; Menke, Michael A.

; Paredy, Dayakar

; Petolino, Joseph F.

; Smith, Kelley

; Woosley, Aaron

; TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DowAgroSciences LLC

; STREET: 9330 Zionsville Road

; CITY: Indianapolis

; STATE: Indiana

; COUNTRY: USA

; ZIP: 46268

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/759,602

; FILING DATE: 16-Jan-2004

; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Kraus, Eric J

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 317 337 5110

; TELEFAX: 317 337 4847

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 9408 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: circular

; MOLECULE TYPE: DNA

; SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-10-759-602-16

Query Match 25.4%; Score 209.2; DB 7; Length 9408;
Best Local Similarity 90.1%; Pred. No. 6.1e-52;
Matches 236; Conservative 0; Mismatches 23; Indels 3; Gaps 1;
Qy 2 TGACCGGTACTCCCAAGTATAAGACACAGCTAAACACACATAATG---CAGTGGTCATG 58
Db 1408 TGACAGTACTCCCAAGTATAAGACACACTAAACACACATAATAATACAGTGGTTATA 1467
Qy 59 TCTAAACATGCTTACCATTTTATGTTATCAATCAATCAAGACATTCATAATTAAGT 118
Db 1468 TCTAAACATGCTTCTTACCATTTCATTTGACCAATTGAACATTAATAAATTAAGT 1527
Qy 119 GACCAATCAGATAGTCTCTGTCGGAATATAGAGCTAAGACACTGTGTCTCGTCAAGA 178

Db 1528 GACCAATCAGTAGCTCTCTGTCGAACATAGAGCTAAGACATTGTGTCTCGTCAAGA 1587
Qy 179 TACATGCTTGTAGATTTTACATTCACCCCTAGACACACTCTAAGACACAACCTTAAG 238
Db 1588 TACATGCTTGTAGATTTTATATATTCACCTCCCAAGACACACTCTAAGACACAACGTAAC 1647
Qy 239 ACACCCATTGTACATGCCCTAA 260
Db 1648 ACACCCATTGTACATGCTCTTA 1669

RESULT 12

US-10-425-115-134827/C

; Sequence 134827, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 134827

; LENGTH: 814

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_54445C.1

US-10-425-115-134827

Query Match 21.8%; Score 179.6; DB 8; Length 814;
Best Local Similarity 93.1%; Pred. No. 1.6e-43;
Matches 188; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 59 TCTAAACATGCTTACCATATTTCATTGTATCAATCAGAACATTCATAATAATTAAAGT 118
Db 814 TGTCTAAACATGCTTTCATCATATTTCATTGACCNTCAAAACATTCATAAATTAAAGT 755
Qy 119 GACCAATCAGATAGTCTCTGTCGGAATATAGAGCTAAGACACTGTGTCTCGTCAAGA 178
Db 754 GACCAATCAGATAGTCTCTGTCGGAATATAGAGCTAAGACACTGTGTCTCGTCAAGA 695
Qy 179 TACATGCTTGTAGATTTTACATTCACCCCTAGACACACTCTAAGACACAACCTTAAG 238
Db 694 TACGTGCTTGTAGATTTTTCATTCACCCCTAGACACACTCTAAGACACAACCTTAAG 635
Qy 239 ACACCCATTGTACATGCCCTAA 260
Db 634 ACACCCATTGTACATGCCCTTA 613

RESULT 13

US-10-425-114-23949/C

; Sequence 23949, Application US/10425114

; Publication No. US20040034888A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E.

; APPLICANT: Tabaska, Jack E.

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 23949

LENGTH: 485
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3606-031-G10_FLI
US-10-425-114-23949

Query Match 21.8%; Score 179.4; DB 7; Length 485;
Best Local Similarity 94.4%; Pred. No. 1.4e-43;
Matches 186; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 64 AACATGTCCTTACCATATTCATTCATCAATCAGAACATTCATCAATTAAGTGACCA 123
Db 481 AAACATGTCCTTATCATATTCATTCATCAATCAATCAATCAATTAAGTGACCA 422

Qy 124 ATCAGATAGTCCTCTGTCCTCCCAATATAGAGCTAGACACTGTCTTCGTCAGATACAT 183
Db 421 ATCAGATAGTCCTCTGTCCTCCCAATATAGAGCTAGACACTGTCTTCGTCAGATACAT 362

Qy 184 GTCTTGAGATTTTACATTCACCCCTCAGACACTCTTAAGACACAACTTAAGACACC 243
Db 361 GTCTTGAGATTTTACATTCACCCCTCAGACACTCTTAAGACACAACTTAAGACACC 302

Qy 244 CATTGTACATGCCCTAA 260
Db 301 CACTGTACATGCCCTTA 285

RESULT 14
US-10-425-115-34629/c
Sequence 34629, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 34629
LENGTH: 379
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)-(379)
OTHER INFORMATION: unsure at all n locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_131586C.1
US-10-425-115-34629

Query Match 21.6%; Score 177.8; DB 8; Length 379;
Best Local Similarity 86.3%; Pred. No. 3.8e-43;
Matches 208; Conservative 0; Mismatches 32; Indels 1; Gaps 1;

Qy 25 CACAGCTAAACACACACATATGAGTGGTGTCTGCTAAACATGCTGTCTTACCATATTC 84
Db 379 CATTAACCTAAACACACACATATATATATGCTGTCTTAAACATATGCTTATCATATTC 320

Qy 85 ATTGTATCAATCAGAACATTCATTAATTAAGTGACCAATCAGATAGTCTCTGTCCTCG 144
Db 319 ATTATACAAATCAGAGCATTCATTAATTAAGTGATCAATCAAAATATCTACTGTCTCG 260

Qy 145 AATATAGAGCTAAGACACTGTCTTCGTCAGATAGTCTTGTGAGATTTTACATTC 204
Db 259 AACATAGAGCTAAGACACTGTCTTCGTCAGATAGTCTTGTGAGTCTTTTAAACATTT 200

Qy 205 ACCCCCTCAGACACTCTTAAGACACAACTTTAAGACACCCCATTTGTACATGCCCTAACTGG 264

Db 199 A-CCCCCTAGACATACCTTACCACCACTTAAACACACTCACTGTATCATGCCATAACGGT 141
Qy 265 C 265
Db 140 C 140

RESULT 15
US-10-425-115-57384
Sequence 57384, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 57384
LENGTH: 443
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_152328C.1
US-10-425-115-57384

Query Match 17.4%; Score 143.2; DB 8; Length 443;
Best Local Similarity 79.7%; Pred. No. 1.4e-32;
Matches 169; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy 62 AAAACATGTCCTTACCATATTCATTCATCAATCAGAACATTCATCAATTAAGTGAC 121
Db 7 AAACATGTCCTTACCATATTCATTCATCAATCAGAGCTTTCATTAATTAAGGAC 66

Qy 122 CAATCAGATAGTCTCTGTCCTCCGATATAGAGCTAAGACACTGTCTTCTGTCAGATAC 181
Db 67 CAATCAGCTAGCTCTTGGCTCAATTTGGAGCTAAACACTGGGTTTTGGGAAAATAC 126

Qy 182 ATGTCTTGAGATTTTACATTCACCCCTCAGACACTCTTAAGACACAACTTTAAGACA 241
Db 127 ATGTTTGGAGTTTTTTTACATCACCCCTTAAACACACTGGGAAAACACAACTTTAAACA 186

Qy 242 CCATTTGATAGCTTCCCTTAATCGCAGCGCTAC 273
Db 187 CCCACTGTATCGCTTGCACAGGGGCCAAAC 218

Search completed: March 5, 2006, 11:26:21
Job time : 825 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 11:08:25 ; Search time 513 Seconds
(without alignments)

3517.379 Million cell updates/sec

Title: US-10-660-208-90

Perfect score: 823

Sequence: 1 ctgacgggtactcaagtat.....cgatccattctccagcgag 823

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 14437070

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New:*

- 1: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	44.6	5.4	393323	7 US-10-330-773-23	Sequence 23, Appl
C 2	37.4	4.5	2010	6 US-09-925-065A-715737	Sequence 715737
C 3	37.4	4.5	2010	6 US-09-925-065A-715738	Sequence 715738
C 4	37.4	4.5	2010	6 US-09-925-065A-715739	Sequence 715739
C 5	36.4	4.4	1148	6 US-09-925-065A-717296	Sequence 717296
C 6	36	4.4	415	6 US-09-925-065A-652867	Sequence 652867
C 7	36	4.4	1829	8 US-10-750-185-64389	Sequence 64389, A
C 8	36	4.4	1829	8 US-10-750-623-64389	Sequence 64389, A
C 9	36	4.4	4149	12 US-11-098-686-9452	Sequence 9452, Ap
C 10	36	4.4	1457619	12 US-11-098-686-8739	Sequence 8739, Ap
C 11	34.8	4.2	904	6 US-09-925-065A-3542	Sequence 3542, Ap
C 12	34.8	4.2	523643	7 US-10-330-773-308	Sequence 308, App
C 13	34.6	4.2	509	6 US-09-925-065A-630175	Sequence 630175
C 14	34.6	4.2	529	6 US-09-925-065A-192068	Sequence 192068
C 15	34.2	4.2	419	6 US-09-925-065A-487029	Sequence 487029
C 16	34.2	4.2	419	6 US-09-925-065A-487030	Sequence 487030
C 17	33.8	4.1	523643	7 US-10-330-773-308	Sequence 308, App
C 18	33.6	4.1	1784	6 US-09-925-065A-671953	Sequence 671953
C 19	33.6	4.1	2759	8 US-10-750-185-34470	Sequence 34470, A
C 20	33.6	4.1	2759	8 US-10-750-623-34470	Sequence 34470, A

C 21	33.6	4.1	6433	7 US-10-330-773-711	Sequence 711, App
C 22	33.6	4.1	121167	7 US-10-330-773-710	Sequence 710, App
C 23	33.4	4.1	521	6 US-09-925-065A-140955	Sequence 140955
C 24	33.4	4.1	540	6 US-09-925-065A-111937	Sequence 111937
C 25	33.2	4.0	459	6 US-09-925-065A-199187	Sequence 199187
C 26	33.2	4.0	536	6 US-09-925-065A-333591	Sequence 333591
C 27	33.2	4.0	551	6 US-09-925-065A-447145	Sequence 447145
C 28	33.2	4.0	560	6 US-09-925-065A-190696	Sequence 190696
C 29	33.2	4.0	573	6 US-09-925-065A-784400	Sequence 784400
C 30	33.2	4.0	618	6 US-09-925-065A-402539	Sequence 402539
C 31	33.2	4.0	615	6 US-09-925-065A-169134	Sequence 169134
C 32	33.2	4.0	640	6 US-09-925-065A-783578	Sequence 783578
C 33	33.2	4.0	1220	6 US-09-925-065A-690610	Sequence 690610
C 34	33.2	4.0	2100	6 US-09-925-065A-720567	Sequence 720567
C 35	33.2	4.0	254396	7 US-10-330-773-534	Sequence 534, App
C 36	33	4.0	388	6 US-09-925-065A-393782	Sequence 393782
C 37	33	4.0	512	6 US-09-925-065A-499969	Sequence 499969
C 38	33	4.0	529	6 US-09-925-065A-192067	Sequence 192067
C 39	33	4.0	588	6 US-09-925-065A-249129	Sequence 249129
C 40	33	4.0	776	6 US-09-925-065A-711775	Sequence 711775
C 41	33	4.0	1020	8 US-10-750-185-49985	Sequence 49985, A
C 42	33	4.0	1020	8 US-10-750-623-49985	Sequence 49985, A
C 43	33	4.0	1272	8 US-10-750-185-51144	Sequence 51144, A
C 44	33	4.0	1272	8 US-10-750-623-51144	Sequence 51144, A
C 45	33	4.0	8537	8 US-10-340-708-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1
US-10-330-773-23/c
; Sequence 23, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 393323
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(393323)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-23

QY	112	TTAAAGTGACCAATCAGATAGTCTCTGTCGCCGAATATAGAGCTAGACACTGTGTCTTC	171
Db	160000	TCAATGTGCTCTTTACATAATATCAAGGCTCTTATTTAACTGGGCATATATCTATGAATA	159941
QY	172	GTCAAGATACATGCTCTTGAGATTTTACATTCACCCCTAGACACACTCTAAGACACA	231
Db	159940	TGTATAGTAGTGTGTTTAAATATTAATAACACACACACACACACACACACA	159881
QY	232	ACTTAAGACACCACTTGTATACATGCCCTAACTGCACCGCTACGTAGGGGCTATTCAAGAA	291
Db	159880	CACACACACACACACTTCTTATGGAAATATATGATGGCTACCTTCAGCTGAAGGAAA	159821
QY	292	CCAACCATGTACAGTTGTTGCAACGTGAATGGTTATTTGCTTCAGATTAAGCTAATTAT	351
Db	159820	GAGATTTCTTCCACTATATAGCAACATCCAAGATGCTTGGTTTAAAAAATAAATAACAAG	159761

QY 352 TTAGACTGATGAGCTGCAATTCATAGACAAAAACAGTGTAGAGCCGTATAGCAATT 411
|||
Db 159760 TTGGCTCTCAATAGCAGTATAAATTAACAAAAATTCAAATTCATAGATCTTG 159701
|||
QY 412 AAGCAACAGCGAA 426
|||
Db 159700 TAACTTAACAGACAA 159686
|||

RESULT 2

US-09-925-065A-715737/c
; Sequence 715737, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 715737
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-715737

Query Match 4.5%; Score 37.4; DB 6; Length 2010;
Best Local Similarity 51.5%; Pred. No. 4.8;
Matches 86; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
QY 262 TGGCACCCTAGTAGGGCTATTCAAGAACCAACATGTACAGTTGTGCAACGTGAAT 321
|||
Db 1856 TGGCAACTACAGTTTGGGCAGTTTGGTAACACCCCTCTCTGCTGCTGCTTTAATAG 1797
|||
QY 322 GGTATTGCTTCAGATTAAAGCTAATTTATTAGACTGATGCACTGCAATTCATAGAGA 381
|||
Db 1796 GTATAATTGACAAATTTGAATTTGTATATATTTAAGGTGTACCATTTGATATTTGATACA 1737
|||
QY 382 CAAAAACAGTGTAGAGCCGTATAGCAATTAAGCAACAAACAGCGAACA 428
|||
Db 1736 TATGTGCTATTGTGGAATAATCACCAGAAATCAAGCTAACTAACCATCA 1690
|||

RESULT 3

US-09-925-065A-715738/c
; Sequence 715738, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766

; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 715738
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-715738

Query Match 4.5%; Score 37.4; DB 6; Length 2010;
Best Local Similarity 51.5%; Pred. No. 4.8;
Matches 86; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
QY 262 TGGCACCCTAGTAGGGCTATTCAAGAACCAACATGTACAGTTGTGCAACGTGAAT 321
|||
Db 1856 TGGCAACTACAGTTTGGGCAGTTTGGTAACACCCCTCTCTGCTGCTGCTTTAATAG 1797
|||
QY 322 GGTATTGCTTCAGATTAAAGCTAATTTATTAGACTGATGCACTGCAATTCATAGAGA 381
|||
Db 1796 GTATAATTGACAAATTTGAATTTGTATATATTTAAGGTGTACCATTTGATATTTGATACA 1737
|||
QY 382 CAAAAACAGTGTAGAGCCGTATAGCAATTAAGCAACAAACAGCGAACA 428
|||
Db 1736 TATGTGCTATTGTGGAATAATCACCAGAAATCAAGCTAACTAACCATCA 1690
|||

RESULT 4

US-09-925-065A-715739/c
; Sequence 715739, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 715739
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-715739

Query Match 4.5%; Score 37.4; DB 6; Length 2010;
Best Local Similarity 51.5%; Pred. No. 4.8;
Matches 86; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
QY 262 TGGCACCCTAGTAGGGCTATTCAAGAACCAACATGTACAGTTGTGCAACGTGAAT 321
|||
Db 1856 TGGCAACTACAGTTTGGGCAGTTTGGTAACACCCCTCTCTGCTGCTGCTTTAATAG 1797
|||
QY 322 GGTATTGCTTCAGATTAAAGCTAATTTATTAGACTGATGCACTGCAATTCATAGAGA 381
|||
Db 1796 GTATAATTGACAAATTTGAATTTGTATATATTTAAGGTGTACCATTTGATATTTGATACA 1737
|||
QY 382 CAAAAACAGTGTAGAGCCGTATAGCAATTAAGCAACAAACAGCGAACA 428
|||
Db 1736 TATGTGCTATTGTGGAATAATCACCAGAAATCAAGCTAACTAACCATCA 1690
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; Sequence 64389, Application US/10750623		; Sequence 64389, Application US/10750623	
; Publication No. US20050287531A1		; Publication No. US20050287531A1	
; GENERAL INFORMATION:		; GENERAL INFORMATION:	
; APPLICANT: MMI GENOMICS, INC.		; APPLICANT: MMI GENOMICS, INC.	
; APPLICANT: DENISE, Sue K.		; APPLICANT: DENISE, Sue K.	
; APPLICANT: KERR, Richard		; APPLICANT: KERR, Richard	
; APPLICANT: ROSENFELD, David		; APPLICANT: ROSENFELD, David	
; APPLICANT: HOLM, Tom		; APPLICANT: HOLM, Tom	
; APPLICANT: BATES, Stephen		; APPLICANT: BATES, Stephen	
; APPLICANT: FANTIN, Dennis		; APPLICANT: FANTIN, Dennis	
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS		; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS	
; FILE REFERENCE: MW11100-1		; FILE REFERENCE: MW11100-1	
; CURRENT APPLICATION NUMBER: US/10/750,623		; CURRENT APPLICATION NUMBER: US/10/750,623	
; CURRENT FILING DATE: 2003-12-31		; CURRENT FILING DATE: 2003-12-31	
; PRIOR APPLICATION NUMBER: US 60/437,482		; PRIOR APPLICATION NUMBER: US 60/437,482	
; PRIOR FILING DATE: 2002-12-31		; PRIOR FILING DATE: 2002-12-31	
; NUMBER OF SEQ ID NOS: 64922		; NUMBER OF SEQ ID NOS: 64922	
; SOFTWARE: PatentIN version 3.1		; SOFTWARE: PatentIN version 3.1	
; SEQ ID NO 64389		; SEQ ID NO 64389	
; LENGTH: 1829		; LENGTH: 1829	
; TYPE: DNA		; TYPE: DNA	
; ORGANISM: Bovine 19866880119920		; ORGANISM: Bovine 19866880119920	
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Matches 90; Conservative 0; Mismatches 90; Indels 0; Gaps 0;		Matches 135; Conservative 0; Mismatches 165; Indels 0; Gaps 0;	
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DB 942 AACTGTATTAACCTGTGGAAGTTTAAATTTTCACTTAAATGGGAATTTATGAATT 1001		DB 680217 ACTGTACAGCAACCTAAACACACAGCAGCACTTGCACTATTACTAAAGAAAGATAGA 680276	
QY 354 AGACTGATGCGCTGCAATTCATAGACACAAACAGTGTAGAACCGGTATTAAGCATTA 413		QY 76 ACCATATTCTATGTATCAATCAGAACATTCATTAATTAAGTGAACCAATCAGATGCT 135	
DB 1002 AGAATATTTTGAAGCAAGTTATTCATATAAACATCACAGAAATGCTTTATTTA 1061		DB 680277 ACACATTGAACCTATAGTAACACAAATGATATACATAAAATAACCTATTAGAGAA 680336	
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; Sequence 9452, Application US/11098686		; Sequence 3542, Application US/09925065A	
; Publication No. US20060024696A1		; Publication No. US20040181048A1	
; GENERAL INFORMATION:		; GENERAL INFORMATION:	
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.		; APPLICANT: Wang, David G.	
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES		; TITLE OF INVENTION: Identification and Mapping of Single	
; FILE REFERENCE: 09531-128001		; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome	
; CURRENT APPLICATION NUMBER: US/11/098,686		; FILE REFERENCE: 108827.135	
; CURRENT FILING DATE: 2005-04-04			
; PRIOR APPLICATION NUMBER: PCT/US03/31318			
; PRIOR FILING DATE: 2003-10-01			
; PRIOR APPLICATION NUMBER: US 60/416,395			
; PRIOR FILING DATE: 2002-10-04			
; NUMBER OF SEQ ID NOS: 11433			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 9452			
; LENGTH: 4149			
; TYPE: DNA			
; ORGANISM: Lawsonia intracellularis			
US-11-098-686-9452			
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Best Local Similarity 45.0%; Pred. No. 1.8e+02;		Best Local Similarity 4.4%; Score 36; DB 12; Length 4149;	
Matches 135; Conservative 0; Mismatches 165; Indels 0; Gaps 0;		Matches 135; Conservative 0; Mismatches 165; Indels 0; Gaps 0;	
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QY 76 ACCATATTCTATGTATCAATCAGAACATTCATTAATTAAGTGAACCAATCAGATGCT 135		QY 76 ACCATATTCTATGTATCAATCAGAACATTCATTAATTAAGTGAACCAATCAGATGCT 135	

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 08:22:14 ; Search time 275 Seconds
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5319.757 Million cell updates/sec

Title: US-10-660-208-90

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Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

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Maximum Match 100%

Listing first 45 summaries

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- 9: /cgn2_6/ptodata/1/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	209.2	25.4	9299	3	US-09-097-319A-15
5	209.2	25.4	9299	3	US-09-097-319A-15
6	209.2	25.4	9408	3	US-09-097-319A-16
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8	110.2	13.4	720	3	US-09-950-933A-8
9	41.6	5.1	601	3	US-09-949-016-160080
10	41.6	5.1	43562	3	US-09-949-016-16222
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12	37.4	4.5	105413	3	US-10-427-923-3
13	37.4	4.5	112219	3	US-09-949-016-12453
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15	37.4	4.5	113186	3	US-09-949-016-17572
16	36.6	4.4	1141	3	US-09-806-708B-22
17	35.4	4.3	132456	3	US-09-949-016-13750
18	34.8	4.2	630	3	US-09-830-230A-56
19	34.8	4.2	690	3	US-09-830-230A-55
20	34.2	4.2	601	3	US-09-949-016-81743
21	34.2	4.2	125192	3	US-09-949-016-14120
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32	33.4	4.1	107045	3	US-09-949-002-772	App
33	33.4	4.1	124701	3	US-09-949-016-11817	A
34	33.4	4.1	124701	3	US-09-949-016-15439	A
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37	33.2	4.0	57751	3	US-09-949-016-13631	A
C 38	33.2	4.0	106256	3	US-09-949-016-16858	A
C 39	33.2	4.0	163662	3	US-09-949-016-12545	A
C 40	33.2	4.0	163664	3	US-09-949-016-13446	A
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43	32.8	4.0	601	3	US-09-949-016-90120	A
44	32.8	4.0	1141	3	US-09-806-708B-22	App1
C 45	32.6	4.0	601	3	US-09-949-016-108444	A

ALIGNMENTS

RESULT 1
US-08-581-148C-30
Sequence 30, Application US/08581148C
Patent No. 6060644
GENERAL INFORMATION:
APPLICANT: Schnable, Patrick S.
APPLICANT: Robertson, Donald S.
APPLICANT: Hansen, Joel D.
APPLICANT: Nikolau, Basil J.
APPLICANT: Xu, Xiaojie
APPLICANT: Xia, Yiji
TITLE OF INVENTION: ISOLATION AND USE OF CUTICULAR LIPID
TITLE OF INVENTION: GENES
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
CITY: Chicago
STATE: IL
COUNTRY: US
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,148C
FILING DATE: 29-DEC-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Larcher, Carol
REGISTRATION NUMBER: 35243
REFERENCE/DOCKET NUMBER: 71380
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 6343 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Zea mays
INDIVIDUAL ISOLATE: Z.mays Glossy2 locus DNA

STATE: Indiana
COUNTRY: USA
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,971
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317 337 4816
TELEFAX: 317 337 4847
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6550 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: exon
LOCATION: 4201..4425
OTHER INFORMATION: /product= "Peroxidase"
FEATURE:
NAME/KEY: intron
LOCATION: 4426..5058
FEATURE:
NAME/KEY: exon
LOCATION: 5059..5250
FEATURE:
NAME/KEY: intron
LOCATION: 5251..5382
FEATURE:
NAME/KEY: exon
LOCATION: 5383..5548
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FEATURE:
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LOCATION: 5650..6065
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NAME/KEY: CDS
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US-09-643-971-1
Query Match 25.4%; Score 209.2; DB 3; Length 6550;
Best Local Similarity 90.1%; Pred. No. 3.4e-59;
Matches 236; Conservative 0; Mismatches 23; Indels 3; Gaps 1;
QY 2 TGCACGGTACTCCAGTATAGACACAGCTAAACACACATATG---CAGTGGTCATG 58
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QY 59 TCTAAACATGTGCTTACCATTATTCATGTCATCAATCAGAACATTCATTAATTAAGT 118
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DB 1475 GACCAATCAGTACGCTCTGTCGCCGAATATAGAGTAAAGACACTGTGCTTCGTCAAGA 1534
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DB 1535 TACATGCTTTAAGTTTTTTTATATTTACTCCCAAGACACACTCTAAGACACAACTTAAG 1594
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DB 1595 ACACCCATTGTACATGCTCTTA 1616
RESULT 4
US-09-097-319A-15
Sequence 15, Application US/09097319A
Patent No. 6384207
GENERAL INFORMATION:
APPLICANT: Ainley, Michael
APPLICANT: Armstrong, Katherine
APPLICANT: Belmar, Scott
APPLICANT: Folkerts, Otto
APPLICANT: Hopkins, Nicole
APPLICANT: Menke, Michael A.
APPLICANT: Parredy, Dayakar
APPLICANT: Petolino, Joseph F.
APPLICANT: Smith, Kelley
APPLICANT: Woosley, Aaron
TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dowelanco Patent Department
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,319A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317 337 4816
TELEFAX: 317 337 4847
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 9299 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA
US-09-097-319A-15
Query Match 25.4%; Score 209.2; DB 3; Length 9299;
Best Local Similarity 90.1%; Pred. No. 4.2e-59;
Matches 236; Conservative 0; Mismatches 23; Indels 3; Gaps 1;
QY 2 TGCACGGTACTCCAGTATAGACACAGCTAAACACACATATG---CAGTGGTCATG 58
DB 1402 TGCACAGTACTCCAGTATAGACACACATATG---CAGTGGTCATG 1461
QY 59 TCTAAACATGTGCTTACCATTATTCATGTCATCAATCAGAACATTCATTAATTAAGT 118
DB 1462 TCTAAACATGTGCTTACCATTATTCATGTCATCAATCAGAACATTCATTAATTAAGT 1521
QY 119 GACCAATCAGATAGTCTCTGTCGCCGAATATAGAGTAAAGACACTGTGCTTCGTCAAGA 178
DB 1522 GACCAATCAGTACGCTCTGTCGCCGAATATAGAGTAAAGACACTGTGCTTCGTCAAGA 1581
QY 179 TACATGCTTGAGATTTTACATTCACCCCTAGACACACTCTAAGACACAACTTAAG 238
DB 1582 TACATGCTTTAAGTTTTTTTATATTTACTCCCAAGACACACTCTAAGACACAACTTAAG 1641
QY 239 ACACCCATTGTACATGCCCTAA 260


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Db 1642 ACACCCATTGTACATGCTCTTA 1663

RESULT 5
US-09-643-971-15
; Sequence 15, Application US/09643971
; Patent No. 669984
; GENERAL INFORMATION:
; APPLICANT: Ainley, Michael
; APPLICANT: Armstrong, Katherine
; APPLICANT: Belmar, Scott
; APPLICANT: Folkerts, Otto
; APPLICANT: Hopkins, Nicole
; APPLICANT: Menke, Michael A.
; APPLICANT: Paredy, Dayakar
; APPLICANT: Petolino, Joseph F.
; APPLICANT: Smith, Kelley
; APPLICANT: Woosley, Aaron
; TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dowelanco Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/643,971
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stuart, Donald R
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317 337 4816
; TELEFAX: 317 337 4847
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9299 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA
; US-09-643-971-15

Query Match 25.4%; Score 209.2; DB 3; Length 9299;
Best Local Similarity 90.1%; Pred. No. 4.2e-59;
Matches 236; Conservative 0; Mismatches 23; Indels 3; Gaps 1;

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Db 1402 TGCACAGTACTCCAAGTATAAGACACAACTAAACACACATAATTAATACAGTGGTTATA 1461
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QY 239 ACACCCATTGTACATGCTCTTA 260
Db 1642 ACACCCATTGTACATGCTCTTA 1663

US-09-097-319A-16
; Sequence 16, Application US/09097319A
; Patent No. 6384207
; GENERAL INFORMATION:
; APPLICANT: Ainley, Michael
; APPLICANT: Armstrong, Katherine
; APPLICANT: Belmar, Scott
; APPLICANT: Folkerts, Otto
; APPLICANT: Hopkins, Nicole
; APPLICANT: Menke, Michael A.
; APPLICANT: Paredy, Dayakar
; APPLICANT: Petolino, Joseph F.
; APPLICANT: Smith, Kelley
; APPLICANT: Woosley, Aaron
; TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dowelanco Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/097,319A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Stuart, Donald R
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317 337 4816
; TELEFAX: 317 337 4847
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9408 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA
; US-09-097-319A-16

Query Match 25.4%; Score 209.2; DB 3; Length 9408;
Best Local Similarity 90.1%; Pred. No. 4.3e-59;
Matches 236; Conservative 0; Mismatches 23; Indels 3; Gaps 1;

QY 2 TGCACGGTACTCCAAGTATAAGACACAGCTAAACACACATAATG---CAGTGGTCATG 58
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Db 1468 TCTAAACATGTGCTTACCATATTTCATTTGATCAATCAGAACATTCAATAAATTAAAGT 1527
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Db 1588 TACATGCTTGAATTTTTTACATTTTACATTTTACATTTTACATTTTACATTTTACATTTAAG 1647
QY 239 ACACCCATTGTACATGCTCTTA 260
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RESULT 7
 US-09-643-971-16
 ; Sequence 16, Application US/09643971
 ; Patent No. 6699984
 ; GENERAL INFORMATION:
 ; APPLICANT: Ainley, Michael
 ; APPLICANT: Armstrong, Katherine
 ; APPLICANT: Belmar, Scott
 ; APPLICANT: Folkerts, Otto
 ; APPLICANT: Hopkins, Nicole
 ; APPLICANT: Menke, Michael A.
 ; APPLICANT: Parredy, Dayakar
 ; APPLICANT: Petolino, Joseph F.
 ; APPLICANT: Smith, Kelley
 ; APPLICANT: Woosley, Aaron
 ; TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
 ; NUMBER OF SEQUENCES: 59
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DowElanco Patent Department
 ; STREET: 9330 Zionsville Road
 ; CITY: Indianapolis
 ; STATE: Indiana
 ; COUNTRY: USA
 ; ZIP: 46268
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/643,971
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Stuart, Donald R
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 317 337 4816
 ; TELEFAX: 317 337 4847
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9408 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: circular
 ; MOLECULE TYPE: DNA
 ; US-09-643-971-16

Query Match 25.4%; Score 209.2; DB 3; Length 9408;
 Best Local Similarity 90.1%; Pred. No. 4.3e-59;
 Matches 236; Conservative 0; Mismatches 23; Indels 3; Gaps 1;
 QY 2 TGCACGGTACTCCAAAGTATAAGACACAGCTAAACACAAACATAATG---CAGTGGTCATG 58
 Db 1408 TGCACAGTACTCCAAAGTATAAGACACAACTAAACACAACTAATAATACAGTGGTTATA 1467
 QY 59 TCTAAACATGTGCTTACCATATTCATTCATCAATCAGACATTCATCAATTAATTAAGT 118
 Db 1468 TCTAAACATGTGCTTACCATATTCATTCATCAATTCAGACATTCATCAATTAATTAAGT 1527
 QY 119 GACCAATCAGATAGTCTCCTGTCCGGAATATAGAGCTAAGACATGCTGCTTCGTCAGA 178
 Db 1528 GACCAATCAGTACGCTCCTGTCTCGACATAGAGCTAAGACATGCTGCTTCGTCAGA 1587
 QY 179 TACATGCTTTGAGATTTTTTACATTCACCCCTTAGACACACTCTAAGACACAACTTAAG 238
 Db 1588 TACATGCTTTAAGTTTTTTTATATTTACTCCCAAGACACACTCTAAGACACAACTTAAG 1647
 QY 239 ACACCCATTGTACATGCCCTAA 260
 Db 1648 ACACCCATTGTACATGCTCTTA 1669

RESULT 8
 US-09-950-933A-8
 ; Sequence 8, Application US/09950933A
 ; Patent No. 6875907
 ; GENERAL INFORMATION:
 ; APPLICANT: Simmons, Carl R.
 ; APPLICANT: Navarro, Pedro
 ; TITLE OF INVENTION: Antimicrobial Peptides and Methods of
 ; TITLE OF INVENTION: Use
 ; FILE REFERENCE: 35718/238472
 ; CURRENT APPLICATION NUMBER: US/09/950,933A
 ; CURRENT FILING DATE: 2001-09-11
 ; PRIOR APPLICATION NUMBER: 60/232,569
 ; PRIOR FILING DATE: 2000-09-13
 ; NUMBER OF SEQ ID NOS: 99
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8
 ; LENGTH: 720
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (119)...(403)
 ; US-09-950-933A-8

Query Match 13.4%; Score 110.2; DB 3; Length 720;
 Best Local Similarity 90.1%; Pred. No. 2.2e-26;
 Matches 118; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 QY 1 CTGCACGGTACTCCAAAGTATAAGACACAGCTAAACACAAACATAATGCAATGTCATGTC 60
 Db 578 CTGCACGGTACTCCAAAGTATAAGACACAACTAAACACAACTAATTAATTAAGTGA 697
 QY 61 TAAACATGTGCTTACCATATTCATTCATCAATCAGACATTCATCAATTAATTAAGTGA 120
 Db 638 TAAACATGTGCTTACCATATTCATTCATCAATCAGACATTCATCAATTAATTAAGTGA 697
 QY 121 CCAATCAGATA 131
 Db 698 CCAAAAAAAAA 708

RESULT 9
 US-09-949-016-160080/c
 ; Sequence 160080, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 160080
 ; LENGTH: 601
 ; TYPE: DNA
 ; ORGANISM: Human
 ; US-09-949-016-160080

Query Match 5.1%; Score 41.6; DB 3; Length 601;
 Best Local Similarity 53.8%; Pred. No. 0.0027;
 Matches 86; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
 QY 246 TTGTACATGCCCTTAAGTGGACCGCTACGTAGGGGCTATTCAAGAACCAACCATGTACAG 305

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Db 241 TTCTCAAGATTAATACTGGGACCATATATGGCAGGCAATTTGAAGAACTTGCTTGCTGAGA 182
Qy 306 TTGTTGCAACGTGAATGTTATTTGCTTCAGATTAAAGCTAATTAATTTAGACTGATGAG 365
Db 181 TTGTAATTCCTTATTATTAGAACGATTCAGATTAGATAAAGCTGCTATTGACAGATGTTG 122
Qy 366 CTGCAATTCATAGACACAAAACAGTGTAGAGCCGTATA 405
Db 121 ATGAGATTCTTTTCAGTGAAGAAAGTAGAGAGGAGTTAAA 82

RESULT 10
US-09-949-016-16222/c
; Sequence 16222, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16222
; LENGTH: 43562
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(43562)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16222

Query Match 5.1%; Score 41.6; DB 3; Length 43562;
Best Local Similarity 53.8%; Pred. No. 0.039;
Matches 86; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

Qy 246 TTGTACATGCCCTACTGCGACCGCTAGTAGGGCTATTCAAGAACCAACCATGTACAG 305
Db 32557 TTCTCAAGATTAATACTGGGACCATATATGGCAGGCAATTTGAAGAACTTGCTTGCTGAGA 32498
Qy 306 TTGTTGCAACGTGAATGTTATTTGCTTCAGATTAAAGCTAATTAATTTAGACTGATGAG 365
Db 32497 TTGTGAATTCCTTATTATTAGAACGATTCAGATTAGATAAAGCTGCTATTGACAGATGTTG 32438
Qy 366 CTGCAATTCATAGACACAAAACAGTGTAGAGCCGTATA 405
Db 32437 ATGAGATTCTTTTCAGTGAAGAAAGTAGAGAGGAGTTAAA 32398

RESULT 11
US-09-949-016-15844
; Sequence 15844, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15844
; LENGTH: 68580
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-15844

Query Match 4.7%; Score 38.4; DB 3; Length 68580;
Best Local Similarity 48.6%; Pred. No. 0.62;
Matches 105; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

Qy 376 TAGAGACAAAACAGTGTAGAACGCGTATAAGCATTAAAGCAAAACAAAGCGAATTTGCTTA 435
Db 19119 TAAAAAATAAACAACACAGAAACCTTTAAACCTTATGTTTACATGAACACACTGGCTG 19178
Qy 436 GCTACAACCAATTTGCTGGGCTTCCATGGGCATCGCAGAAAGTATTGGCTGCAATATTC 495
Db 19179 TGCCATCATTTTACTGAAAAAGTACCAGGTATGATATAAATAATATATAAATATATTTTC 19238
Qy 496 TGAATTTATAGCGAGGCGCCCAAGCCCATCATTCTCGAGGTGAGCATTTGACTTTT 555
Db 19239 TAAATACATTCCTTCTTACCAGGCACCTTAAAAACCTGTTGTAGCTTAACTTCTAATGAT 19298
Qy 556 GTTAAACGCTCTCGATAAAATTTGTTTCACCTTAAAAATAGA 591
Db 19299 GTTAAATGACTTGATCAACATTTGCATTTGAATAACA 19334

RESULT 12
US-10-427-923-3
; Sequence 3, Application US/10427923
; Patent No. 6916643
; GENERAL INFORMATION:
; APPLICANT: NEELAM, Beena et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001365
; CURRENT APPLICATION NUMBER: US/10/427,923
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 105413
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(105413)
; OTHER INFORMATION: n = A,T,C or G
US-10-427-923-3

Query Match 4.5%; Score 37.4; DB 3; Length 105413;
Best Local Similarity 49.2%; Pred. No. 1.8;
Matches 98; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

Qy 4 CACGGTACTCCAAGTATTAAGACACAGCTAAACACACACATTAATGCAGTGGTCATGCTAA 63
Db 60593 CATAGTATATAATATAATATAATATATATATATATATATATATATATATATATATAT 60652
Qy 64 AACATGTGCTTACCATATTCATTGTATCAATCAGAACATTCATATAAATAAAGTGACCA 123
Db 60653 CACATAGTATATAATATAATATAATATATATATATATATATATATATATATATATAT 60712
Qy 124 ATCAGATAGTCTCCTGTCGCCGAATATAGAGCTAGACACTGTGCTTCTGCTCAAGATACAT 183
Db 60713 ATCAGATAGTATATAATATAATATAATATATATATATATATATATATATATATATAT 60772
Qy 184 GCTTTGAGATTTTTTACAT 202
Db 60773 ATCAGATAGTATATAATAT 60791
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RESULT 13

US-09-949-016-12453
; Sequence 12453, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF.
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12453
; LENGTH: 112219
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(112219)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12453

Query Match 4.5%; Score 37.4; DB 3; Length 112219;
Best Local Similarity 49.2%; Pred. No. 1.8; Indels 0; Gaps 0;
Matches 98; Conservative 0; Mismatches 101;
QY 4 CACGGTACTCCAAGTATAAGACACAGCTAAACACACATAATGCAGTGGTCAATGCTAA 63
DB 60575 CATAGTATAATAATATAATATATATATATATATATATATATATATATATATAT 60634
QY 64 AACATGCTTACCATTATCATCAATCAGAACATCAATAAATTAAGTGACCA 123
DB 60635 CACATAGTATAATAATATATATATATATATATATATATATATATATATATAT 60694
QY 124 ATCAGATAGTCTCTGTCGCCGAATATAGAGCTAAGACACTGTGCTTCGTCGAAGATACAT 183
DB 60695 ATCAGATAGTATAATAATATATATATATATATATATATATATATATATATATAT 60754
QY 184 GTCTTGAGATTTTTTACAT 202
DB 60755 ATCAGATAGTATAATAAT 60773

RESULT 14

US-09-949-016-14324
; Sequence 14324, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14324
; LENGTH: 112222

; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(112222)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14324

Query Match 4.5%; Score 37.4; DB 3; Length 112222;
Best Local Similarity 49.2%; Pred. No. 1.8; Indels 0; Gaps 0;
Matches 98; Conservative 0; Mismatches 101;
QY 4 CACGGTACTCCAAGTATAAGACACAGCTAAACACACATAATGCAGTGGTCAATGCTAA 63
DB 60575 CATAGTATAATAATATAATATATATATATATATATATATATATATATATATAT 60634
QY 64 AACATGCTTACCATTATCATCAATCAGAACATCAATAAATTAAGTGACCA 123
DB 60635 CACATAGTATAATAATATATATATATATATATATATATATATATATATATAT 60694
QY 124 ATCAGATAGTCTCTGTCGCCGAATATAGAGCTAAGACACTGTGCTTCGTCGAAGATACAT 183
DB 60695 ATCAGATAGTATAATAATATATATATATATATATATATATATATATATATATAT 60754
QY 184 GTCTTGAGATTTTTTACAT 202
DB 60755 ATCAGATAGTATAATAAT 60773

RESULT 15

US-09-949-016-17572
; Sequence 17572, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17572
; LENGTH: 113186
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17572

Query Match 4.5%; Score 37.4; DB 3; Length 113186;
Best Local Similarity 49.2%; Pred. No. 1.8; Indels 0; Gaps 0;
Matches 98; Conservative 0; Mismatches 101;
QY 4 CACGGTACTCCAAGTATAAGACACAGCTAAACACACATAATGCAGTGGTCAATGCTAA 63
DB 61562 CATAGTATAATAATATAATATATATATATATATATATATATATATATATATAT 61621
QY 64 AACATGCTTACCATTATCATCAATCAGAACATCAATAAATTAAGTGACCA 123
DB 61622 CACATAGTATAATAATATATATATATATATATATATATATATATATATATAT 61681
QY 124 ATCAGATAGTCTCTGTCGCCGAATATAGAGCTAAGACACTGTGCTTCGTCGAAGATACAT 183
DB 61682 ATCAGATAGTATAATAATATATATATATATATATATATATATATATATATATAT 61741
QY 184 GTCTTGAGATTTTTTACAT 202
DB 61742 ATCAGATAGTATAATAAT 61760

Search completed: March 5, 2006, 08:57:49
Job time : 278 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 10:15:23 ; Search time 4128 Seconds
(without alignments)
9327.948 Million cell updates/sec

Title: US-10-660-208-90

Perfect score: 823

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Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: gb_est5.*
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7: gb_est7.*
8: gb_est8.*
9: gb_est9.*
10: gb_est10.*
11: gb_est11.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	564	68.5	901	10 CG011145	CG011145 ZUAGI45TH
2	256.4	31.2	853	9 BZ818599	BZ818599 PUFAM82TB
3	256.4	31.2	854	9 BZ818600	BZ818600 PUFAM82TB
4	252	30.6	679	9 CC331420	CC331420 OGBMK41TV
5	251.8	30.6	847	10 CW009430	CW009430 ZMBL001
6	251.8	30.6	863	10 CG175756	CG175756 PUFJ20TD
7	250.4	30.4	695	10 CW007582	CW007582 ZMBL000
8	250.4	30.4	777	10 CW006373	CW006373 ZMBL000
9	250.4	30.4	902	9 CC607552	CC607552 OGBUN60TV
10	249.6	30.3	735	9 BZ950843	BZ950843 PUGFN02TB
11	249	30.3	979	10 CL984256	CL984256 ZMBH000
12	248.8	30.2	893	10 CZ362236	CZ362236 ZMBF0140
13	248.8	30.2	894	9 CC356660	CC356660 PUHQX61TD
14	248.2	30.2	717	9 CC397968	CC397968 PUHDC37TD
15	248.2	30.2	769	9 CC397966	CC397966 PUHDC37TB
16	248	30.1	737	9 CC409551	CC409551 PUDJ079TD
17	246.4	29.9	729	10 CG132878	CG132878 PUILN19TD
18	245.6	29.8	882	10 CG130321	CG130321 PUKDM45TB
19	241.2	29.3	924	10 CG017066	CG017066 ZUAA19TV
20	240.8	29.3	557	9 CC033235	CC033235 3591.1.62
21	240.8	29.3	646	9 CC384946	CC384946 PUEH22TD
22	240	29.2	868	9 BZ817311	BZ817311 PUGCL66TD

C 23	240	29.2	985	9 BZ817308	BZ817308 PUGCL66TB
C 24	239	29.0	773	9 BZ795967	BZ795967 PUFEP13TD
C 25	237.6	28.9	687	10 CW014489	CW014489 ZMMBL000
C 26	237.6	28.9	1112	10 CL984622	CL984622 ZMMH0000
C 27	237.4	28.8	635	10 CG119014	CG119014 PUJBF49TB
C 28	234.4	28.5	875	9 BZ993516	BZ993516 PUDDG29TD
C 29	234.4	28.5	876	9 BZ992817	BZ992817 PUDDG28TD
C 30	234.4	28.5	908	9 CC780832	CC780832 ZMMB0C043
C 31	233.6	28.4	1015	10 CG130320	CG130320 PUKDM45TB
C 32	233.2	28.3	733	10 CZ915233	CZ915233 4013010E1
C 33	233.2	28.3	905	10 CG065264	CG065264 PUFF072TD
C 34	233.2	28.3	1030	10 CW000997	CW000997 ZMMBH000
C 35	233	28.3	830	9 CC002788	CC002788 PUDHJ32TD
C 36	232.8	28.3	621	9 BZ791746	BZ791746 PUFH12TD
C 37	232.8	28.3	775	10 CW018123	CW018123 ZMMBL001
C 38	232.8	28.3	897	10 CW010050	CW010050 ZMMBL000
C 39	231	28.1	749	8 DN208175	DN208175 MEST866 B
C 40	229.6	27.9	772	9 BZ994616	BZ994616 PUGGW06TD
C 41	229.6	27.9	780	10 CG038335	CG038335 PUJF77TB
C 42	229.4	27.9	855	10 CG144450	CG144450 PUFKY41TD
C 43	228.6	27.8	1043	10 CG043190	CG043190 PUIDN37TB
C 44	228	27.7	854	10 CG107530	CG107530 PUILN19TD
C 45	227.6	27.7	448	9 BH234262	BH234262 1006178D0

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
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Genomic survey sequence.
CG011145
ACCESSION
CG011145
VERSION
CG011145.1
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1 (bases 1 to 901)
Auker, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: ZUAGI45TV
CONTACT: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
FEATURES
Location/Qualifiers
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/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBPa0060H17"
/clone_lib="ZM_3.0.4.0_KB"
/note="Vector: pBGSK-; Site 1: HincII; 3-4 kb 'unfiltered' genomic DNA library"

ORIGIN
Query Match 68.5%; Score 564; DB 10; Length 901;
Best Local Similarity 99.1%; Pred. No. 1.7e-156;
Matches 567; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 252 ATGCCCTAACTGGCAGCGCTAGTAGGGGCTATTTCAGAACCAACCATGATGTTG 311

		81	Db	ATGGCTTAAC TCGSCACCGCTACGTAGGGGCTATTCAAGAACC AACAAATGTACAGTTGTTG 140
		312	Qy	C A A C G T G A A T G G T A T T T T G C T T C A G A T T A A A G C T A A T T A T T T A G A C T G A T C G A G C T G C A A 371
		141	Db	C A A C G T G A A T G G T A T T T T G C T T C A G A T T A A A G C C A A T T G T T T A G A C T G A T C G A G C T G C A A 200
		372	Qy	T T C A T A G A G A C A A A A C A A G T G T A G A G C C G T A T A A G C A T T A A G C A A A C A A G C G A C A C T T G 431
		201	Db	T T C A T A G A G A C A A A A C A A G T G T A G A G C C G T A T A A G C A T T A A G C A A A C A A G C G A C A C T T G 260
		432	Qy	C T T A G C T A C A A C A A T T T T G C T G G G C T T C C A T G G S C A T C G C A G A A G T A T T G T G G C T G C A T A 491
		261	Db	C T T A G C T A C A A C A A T T T T G C T G G G C T T C C A T G G S C A T C G C A G A A G T A T T G T G G C T G C A T A 320
		492	Qy	T T G C T G A A A T T A T A G C G A G G G C C C A A G S C C C A T C A C T T C A T T C G A G G T C A G C A T T G T A C 551
		321	Db	T T G C T G A A A T T A T A G C G A G G G C C C A A G S C C C A T C A C T T C A T T C G A G G T C A G C A T T G T A C 380
		552	Qy	T T T T G T T A A C G T C T C G A T A A A T T T G T T C A C T T A A A T A G A C C A G T T C A A T T C T G G T T C T A 611
		381	Db	T T T T G T T A A C G T C T C G A T A A A T T T G T T C A C T T A A A T A G A C C A G T T C A A T T C T G G T T C T A 440
		612	Qy	G T C A A C A T C G C T G G A T C C A C G S G G G A G C G A G A C G A A T G T G T G S C C C G C C G C A G T G A G 671
		441	Db	G T C A A C A T C G C T G G A T C C A C G S G G G A G C G A G A C G A A T G T G T G S C C C G C C G C A G T G A G 500
		672	Qy	G C C A A G C G A G C C G G T C G T C G G T C C A A C A C C C C C T C G T T T A T A C T A T A T A T A C A C A G A 731
		501	Db	G C C A A G C C G A G C C G G T C G T C G G T C C A A C C A C C C C C T C G T T T A T A C T A T A T A T A C A C A G A 560
		732	Qy	C G C A G A T A C C C A T A C T G T G T G T G T A G A A G C A A C T G A A A A C A G C C G A G G A T C C T C C T C T C 791
		561	Db	C G C A C G A T A C C A T A C T G T G T G T G T A G A A G C A A C T G A A A C A G C C G A G G A T C C T C C T C T C 620
		792	Qy	C C T C C C C T C C C G A T C C A T T C T C A G C G C A G 823
		621	Db	C C T C T C C C T C T C C G A T C C A T T C T C A G C G C A G 652

RESULT 2	BZ818599	LOCUS	DEFINITION	BZ818599	853 bp	DNA	linear	GSS 18-MAR-2003
				PUFAM82TB	2M	0.6	1.0	KB
								Zea mays genomic clone ZMMBPa275M19,
								genomic survey sequence.

ORGANISM: Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

TITLE	JOURNAL	COMMENT
Maize Genomics Consortium	Unpublished (2003)	Other GSSs: PUFAM82TD

TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel.: 301-838-5843
Fax: 301-838-0208

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FEATURES
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  location/Qualifiers

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ORIGIN

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Best Local Similarity	92.8%	Pred. No. 9e-65		
Matches 269	Conservative 0	Mismatches 21	Indels 0	Gaps 0
Qy	1	CTGCACGGTACTCCAAAGTATAAAGACACAGCTAAACACACATAAATGCACTGTCATGTC	60	
Db	333	CTGCACGGTACTCCAAAGTATAAAGACACAGCTAAACACACATAAATGCACTGTCATGTC	392	
Qy	61	TAAACATGTGCTTACCATATTCATTGTATCNAATCAGAACATTCNAATTAATTAAGTGA	120	
Db	393	TAAACATGTGCTTACCATATTCATTGTATTCACCAATCAGAACATTCNAATTAATTAAGTGA	452	
Qy	121	CCAATCAGATAGTCTCCTGTCCCGAATATAGAGCTAAGACACATGTGTCCTTCGTCGAAGATA	180	
Db	453	CCAATCAGATAGTCTCCTGTCTCGAATATAGAGCTAAGACACATGTGTCCTTCGTCGAAGATA	512	
Qy	181	CATGCTTGAGATTTTTTATCATTCACCCCCCTAGACACACTCTTAAGACACAACTTAAGAC	240	
Db	513	CGTGTCTTGAGATTTTTTATCATTCACCCCCCTAGACACACTCTTAAGACACAACTTAAGAC	572	
Qy	241	ACCATTGTACATGCCCTTAACCTGGCACCGCTAGCTAGGGGGCTATTCAAGA	290	
Db	573	ACTCCATCTTATCATGCTCTTATGATGCTGCTCAATATCATGAGGCAACACGAAAT	632	

RESULT 3
BZ818600/c

SOURCE	ORGANISM
Zea mays	Eukaryote, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

TITLE	COMMENT
Maize Genomics Consortium	
Unpublished (2003)	
Other_GSSs: PUFAM82TB	

TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208

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source
1. .854
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"

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cot selected genomic DNA library"

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ORIGIN

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Best Local Similarity 92.8%; Pred. No. 9e-65;
Matches 269; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 CTGCACGGTACTCCAAGTATAAGACACAGCTAAACACACATTAATCCAGTGGTCATGTC 60
DB 771 CTGCACGGTACTCCAAGTATAAGACACAGCTAAACACACATTAATCCAGTGGTCATGTC 712

QY 61 TAAACACATGTGCTTACCATTATTCATTTGATCAATCAGAAACATTCATAAATTAAGTGA 120
DB 711 TAAACACATGTGCTTACCATTATTCATTTGATCAATCAGAAACATTCATAAATTAAGTGA 652

QY 121 CCAATCAGATAGTCTCTGTCGCCGAATATAGAGCTAAAGACACTGTGTCGTCGAAGATA 180
DB 651 CCAATCAGATAGTCTCTGTCGCCGAATATAGAGCTAAAGACACTGTGTCGTCGAAGATA 592

QY 181 CATGCTCTTGAGATTTTATACCATATTCATTTGATCAATCAGAAACATTCATAAATTAAGTGA 240
DB 591 CGTGTCTTGAGATTTTATACCATATTCATTTGATCAATCAGAAACATTCATAAATTAAGTGA 532

QY 241 ACCATTGTACATGCCCTTAATCTGACCGCTAGCTAGGGCTATTCAAGA 290
DB 531 ACCACTGTACATGCCCTTATAGTGTGTCATATCAGGGCAACGAAA 482

RESULT 4
LOCUS CC331420 679 bp DNA linear GSS 16-MAY-2003
DEFINITION OGMK41TV_ZM_0.7_1.5_KB_Zea_mays_genomic_clone_ZMMBLa0384G09,
genomic survey sequence.
ACCESSION CC331420
VERSION CC331420.1 GI:30800591
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 679)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nurnberg,A., Robbins,D. and Lakey,N.
TITLE Consortium for Maize Genomics
JOURNAL Unpublished (2002)
COMMENT Contact: Cathy Whitelaw
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: methylation filtered.
FEATURES
source
1..679
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone_lib="ZMMBLa0384G09"
/clone_lib="ZM_0.7_1.5_KB"
/notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

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Best Local Similarity 98.1%; Pred. No. 1.8e-63;
Matches 255; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CTGCACGGTACTCCAAGTATAAGACACAGCTAAACACACATTAATCCAGTGGTCATGTC 60
DB 118 CTGCACGGTACTCCAAGTATAAGACACAGCTAAACACACATTAATCCAGTGGTCATGTC 177

QY 61 TAAACACATGTGCTTACCATTATTCATTTGATCAATCAGAAACATTCATAAATTAAGTGA 120

DB 178 TAAACACATGTGCTTACCATTATTCATTTGATCAATCAGAAACATTCATAAATTAAGTGA 237

QY 121 CCAATCAGATAGTCTCTGTCGCCGAATATAGAGCTAAAGACACTGTGTCGTCGAAGATA 180
DB 238 CCAATCAGATAGTCTCTGTCGCCGAATATAGAGCTAAAGACACTGTGTCGTCGAAGATA 297

QY 181 CATGCTCTTGAGATTTTATACCATATTCATTTGATCAATCAGAAACATTCATAAATTAAGTGA 240
DB 298 CATGCTCTTGAGATTTTATACCATATTCATTTGATCAATCAGAAACATTCATAAATTAAGTGA 357

QY 241 ACCATTGTACATGCCCTTAA 260
DB 358 ACCACTGTACATGCCCTTAA 377

RESULT 5
LOCUS CW009430 847 bp DNA linear GSS 23-SEP-2004
DEFINITION ZMMBLa0012C07.r_ZMMBLa_Zea_mays_genomic_clone_ZMMBLa0012C07_3',
genomic survey sequence.
ACCESSION CW009430
VERSION CW009430.1 GI:52592072
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 847)
AUTHORS Wing,R., Luo,M., Soderlund,C. and Haller,K.
TITLE ZMML sequences
JOURNAL Unpublished (2004)
COMMENT Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
Plate: 0012 row: C column: 07
Class: BAC ends.
FEATURES
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Location/Qualifiers
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/cultivar="B73"
/db_xref="taxon:4577"
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/tissue_type="immature ears"
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/note="Vector: pAGIBAC1; Site_1: SalI; Site_2: SalI"

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Query Match 30.6%; Score 251.8; DB 10; Length 847;
Best Local Similarity 93.9%; Pred. No. 2.1e-63;
Matches 262; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 CTGCACGGTACTCCAAGTATAAGACACAGCTAAACACACATTAATCCAGTGGTCATGTC 60
DB 47 CTGCACGGTACTCCAAGTATAAGACACAGCTAAACACACATTAATCCAGTGGTCATGTC 106

QY 61 TAAACACATGTGCTTACCATTATTCATTTGATCAATCAGAAACATTCATAAATTAAGTGA 120
DB 107 TAAACACATGTGCTTACCATTATTCATTTGATCAATCAGAAACATTCATAAATTAAGTGA 166

QY 121 CCAATCAGATAGTCTCTGTCGCCGAATATAGAGCTAAAGACACTGTGTCGTCGAAGATA 180
DB 167 CCAATCAGATAGTCTCTGTCGCCGAATATAGAGCTAAAGACACTGTGTCGTCGAAGATA 226

QY 181 CATGCTCTTGAGATTTTATACCATATTCATTTGATCAATCAGAAACATTCATAAATTAAGTGA 240
DB 227 CATGCTCTTGAGATTTTATACCATATTCATTTGATCAATCAGAAACATTCATAAATTAAGTGA 286


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LOCUS
DEFINITION ZM007582 695 bp DNA linear GSS 23-SEP-2004
ZM007582 genomic survey sequence.
ACCESSION ZM007582
VERSION ZM007582.1 GI:52588391
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 695)
AUTHORS Wing, R., Luo, M., Soderlund, C. and Haller, K.
TITLE ZM007582 sequences
JOURNAL Unpublished (2004)
COMMENT Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
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Class: BAC ends.
FEATURES
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Location/Qualifiers
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/cultivar="B73"
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/note="Vector: PACIBAC1; Site_1: SalI; Site_2: SalI"
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Best Local Similarity 97.7%; Pred. No. 5.3e-63;
Matches 254; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 CTGCACGGTACTCCAGTATTAAGACACAGCTAAACACACATTAATGCGTGGTCAATGTC 60
Db 256 CTGCACGGTACTCCAGTATTAAGACACAGCTAAACACACATTAATGCGTGGTCAATGTC 315
Qy 61 TAAACATGCTCTTACCATATTCATTGTATCATCATGAGACATTCATTAATTAAGTGA 120
Db 316 TAAACATGCTCTTACCATATTCATTGTATCATCATGAGACATTCATTAATTAAGTGA 375
Qy 121 CCAATCAGATAGTCTCTGCTCCGAAATATAGAGCTAAGACACACTGTGCTTCGTCAGGATA 180
Db 376 CCAATCAGATAGTCTCTGCTCCGAAATATAGAGCTAAGACACACTGTGCTTCGTCAGGATA 435
Qy 181 CATGCTTTGAGATTTTACATTCACCCCTAGACACACTCTTAAGACACAACTTAAGAC 240
Db 436 CATGCTTTGAGATTTTACATTCACCCCTAGACACACTCTTAAGACACAACTTAAGAC 495
Qy 241 ACCCATGTTACATGCCCTAA 260
Db 496 ACCCATGTTACATGCCCTAA 515
RESULT 8
LOCUS ZM006373 777 bp DNA linear GSS 23-SEP-2004
ZM006373 genomic survey sequence.
ACCESSION ZM006373
VERSION ZM006373.1 GI:52585956
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 777)
AUTHORS Wing, R., Luo, M., Soderlund, C. and Haller, K.
TITLE ZM006373 sequences
JOURNAL Unpublished (2004)
COMMENT Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
Plate: 0009 row: E column: 11
Class: BAC ends.
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/lab_host="DH10B T1 phage resistant"
/clone_lib="ZM006373"
/note="Vector: PACIBAC1; Site_1: SalI; Site_2: SalI"
ORIGIN
Query Match 30.6%; Score 251.8; DB 10; Length 777;
Best Local Similarity 93.9%; Pred. No. 2.1e-63;
Matches 262; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
Qy 1 CTGCACGGTACTCCAGTATTAAGACACAGCTAAACACACATTAATGCGTGGTCAATGTC 60
Db 359 CTGCACGGTACTCCAGTATTAAGACACAGCTAAACACACATTAATGCGTGGTCAATGTC 418
Qy 61 TAAACATGCTCTTACCATATTCATTGTATCATCATGAGACATTCATTAATTAAGTGA 120
Db 419 TAAACATGCTCTTACCATATTCATTGTATCATCATGAGACATTCATTAATTAAGTGA 478
Qy 121 CCAATCAGATAGTCTCTGCTCCGAAATATAGAGCTAAGACACACTGTGCTTCGTCAGGATA 180
Db 479 CCAATCAGATAGTCTCTGCTCCGAAATATAGAGCTAAGACACACTGTGCTTCGTCAGGATA 538
Qy 181 CATGCTTTGAGATTTTACATTCACCCCTAGACACACTCTTAAGACACAACTTAAGAC 240
Db 539 CATGCTTTGAGATTTTACATTCACCCCTAGACACACTCTTAAGACACAACTTAAGAC 598
Qy 241 ACCCATGTTACATGCCCTAACTGGCAGCTACGAGG 279
Db 599 ACCCATGTTACATGCCCTAACTGGCAGCTACGAGG 637
RESULT 7
LOCUS ZM007582
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
1 (bases 1 to 777)
Wing, R., Luo, M., Soderlund, C. and Haller, K.

TITLE
ZMBL sequences

JOURNAL
Unpublished (2004)

COMMENT
Contact: Rod A. Wing

Arizona Genomics Institute

University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9595

Fax: 520 621 1259

Email: rwing@genome.arizona.edu

Plate: 0007 row: D column: 24

Class: BAC ends.

Location/Qualifiers

1. 777

/organism="Zea mays"

/mol_type="genomic DNA"

/cultivar="B73"

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/clone="ZMBL0007D24"

/tissue type="immature ears"

/lab host="DH10B T1 phage resistant"

/clone lib="ZMBL0a"

/note="Vector: pGIBAC1; Site_1: SalI; Site_2: SalI"

FEATURES

source

Query Match 30.4%; Score 250.4; DB 10; Length 777;
Best Local Similarity 97.7%; Pred. No. 5.5e-63;
Matches 254; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

ORIGIN

1 CTGCACGGTACTCCAAAGTATAAGACACAGCTAAACACACATTAATCGAGTGGTCATGTC 60
263 CTGCACGGTACTCCAAAGTATAAGACACAGCTAAACACACATTAATCGAGTGGTCATGTC 322
61 TAAACATGCTGTCTTACCATATTCATTGTATCAATCAGAACATTCATTAATAAAGTGA 120
323 TAAACATGCTGTCTTACCATATTCATTGTATCAATCAGAACATTCATTAATAAAGTGA 382
121 CCAATCAGATAGTCTCTGTCGCCGAATATAGAGCTAAAGACACTGTGCTTCGTCAGATA 180
383 CCAATCAATAGTCTCTGTCGCCGAATATAGAGCTAAAGACACTGTGCTTCGTCAGATA 442
181 CATGCTCTGAGATTTTACATTCACCCCTAGACACACTCTTAAGACACAACTTAAGAC 240
443 CATGCTCTGAGATTTTACATTCACCCCTAGACACACTCTTAAGACACAACTTAAGAC 502
241 ACCCATGTACATGCCCTAA 260
503 ACCCATGTACATGCCCTAA 522

RESULT 9

CC607552

LOCUS

OSUBN60TV_ZM_0.7_1.5_KB Zea mays genomic clone ZMBM0401J24, linear GSS 18-JUN-2003

DEFINITION

genomic survey sequence.

ACCESSION

CC607552

VERSION

CC607552.1 GI:31968973

KEYWORDS

GSS.

SOURCE

Zea mays

Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 902)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,

Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,

Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics

Unpublished (2002)

Other_GSSs: OGUBN60TH

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TF

Class: methylation filtered.

Location/Qualifiers

1. 902

/organism="Zea mays"

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/db_xref="taxon:4577"

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/clone lib="ZM_0.7_1.5_KB"

/notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb

methylation filtered genomic DNA library"

FEATURES

source

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Best Local Similarity 97.7%; Pred. No. 5.6e-63;
Matches 254; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

ORIGIN

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361 CTGCACGGTACTCCAAAGTATAAGACACAGCTAAACACACATTAATCGAGTGGTCATGTC 420
61 TAAACATGCTGTCTTACCATATTCATTGTATCAATCAGAACATTCATTAATAAAGTGA 120
421 TAAACATGCTGTCTTACCATATTCATTGTATCAATCAGAACATTCATTAATAAAGTGA 480
121 CCAATCAGATAGTCTCTGTCGCCGAATATAGAGCTAAAGACACTGTGCTTCGTCAGATA 180
481 CCAATCAATAGTCTCTGTCGCCGAATATAGAGCTAAAGACACTGTGCTTCGTCAGATA 540
181 CATGCTCTGAGATTTTACATTCACCCCTAGACACACTCTTAAGACACAACTTAAGAC 240
541 CATGCTCTGAGATTTTACATTCACCCCTAGACACACTCTTAAGACACAACTTAAGAC 600
241 ACCCATGTACATGCCCTAA 260
601 ACCCATGTACATGCCCTAA 620

RESULT 10

BZ960843/c

LOCUS

PUGFN02TB_ZM_0.6_1.0_KB Zea mays genomic clone ZMBM0372B04, linear GSS 25-MAR-2003

DEFINITION

genomic survey sequence.

ACCESSION

BZ960843

VERSION

BZ960843.1 GI:29175935

KEYWORDS

GSS.

SOURCE

Zea mays

Zea mays

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 735)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,

Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and

Bennetzen, J.

Maize Genomics Consortium

Unpublished (2003)

Other_GSSs: PUGFN02TD

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TR

Class: sheared ends.

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Best Local Similarity 96.2%; Pred. No. 1.5e-62;
Matches 255; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

1 CTGCACGGTACTCCAAAGTATAAGACACAGCTAAACACACACATAAATGCGTGTGTCATGTC 60
260 CTGCACGGTACTCCAAAGTATAAGACACAGCTAAACACACACATAAATGCGTGTGTC 319
61 TAAACATGTTGTTTACCATATTCATTTATCATCATGATGATGATGATGATGATGATGATG 120
320 TAAACATGTTGTTTACCATATTCATTTATCATCATGATGATGATGATGATGATGATGATG 379
121 CCAATCAGATAGTCTCTGTCCTCCGATATAGAGCTAAGACACTGTGTCCTGTCGAAGATA 180
380 CCAATCAGATAGTCTCTGTCCTCCGATATAGAGCTAAGACACTGTGTCCTGTCGAAGATA 439
181 CATGCTTGGAGATTTTACATTCACCCCTAGACACACTCTTAAGACACAACTTAAGAC 240
440 CGTGTCTTGAGATTTTACATTCACCCCTAGACACACTCTTAAGACACAACTTAAGAC 499
241 ACCCATTTGATGCGCCCTAACTGGC 265
500 ACCCATTTGATGCGCCCTAACTGGC 524

RESULT 12
CZ362236 893 bp DNA linear GSS 29-MAR-2005
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survey sequence.
ACCESSION CZ362236
VERSION CZ362236.1 GI:61972180
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 893)
AUTHORS Bharti,A.K., Nelson,A.B., Young,S., Kaizer,G., Zohovetz,V., Fuks,G.
and Messing,J.
TITLE Construction, Sequencing and Characterization of a Fosmid Library
of the B73 Maize Genome
JOURNAL Unpublished (2005)
COMMENT Contact: Bharti,A.K.
Dr. Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Freelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: SP6
Class: fosmid ends.
Location/Qualifiers
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/mol_type="genomic DNA"
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ORIGIN
Query Match 30.2%; Score 248.8; DB 10; Length 893;

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Db	93	CATGTCCTTGAGATTTTTCATTCATTCACCCCCCTAGACACACTCTTAAGACACACAACTTAAGAC	34
Qy	241	ACCATTGTACATGCCCTAA	260
Db	33	ACCACCTGTACATGCCCTTA	14

RESULT 14
CC397968
LOCUS
DEFINITION PHRD37TD ZM_0.6_1.0 KB Zea mays genomic clone ZMBrA424G01,
genomic survey sequence.
ACCESSION CC397968
VERSION CC397968.1 GI:30878058
717 bp DNA linear GSS 19-MAY-2003

Zea mays
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1. (bases 1 to 717)
 WhiteIaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
 Reenick,A., Fraser,C.N., Yuan,Y., San Miguel,P., Ma,J. and
 Bennetzen,J.
 TITLE
 Maize Genomics Consortium
 Unpublished (2003)
 Other GSSE: PUHDC37TB
 Contact: Cathy WhiteIaw
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whiteIaw@tigr.org
 Seq primer: TP
 Class: sheared ends.
 Location/Qualifiers
 1..717
 /organism="Zea mays"
 FEATURES
 source

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Query Match	30.2%; Score 248.2; DB 9; Length 717;
Best Local Similarity	96.9%; Pred.No. 2.4e-62;
Matches 253; Conservative	0; Mismatches 8; Indels 0; Gaps 0;
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Dd	362 CTGCACGGTACTCCAAGTATAAAGCACAGCTAAACACAACAATTAATGCGTGTCATGTCC 421
Qy	61 TAAAACATGTGCTTTACCATTATCATTGTATCAATCAGAACAATTCATAAATTAAGTGA 120
Dd	422 TAAAACATGTGCTTTACCATTATCATTGTACCAATCANAAACATTCATAAATTAAGTGA 481
Qy	121 CCAATCAGATAGTCTCCTGTGCCGAATATAGAGCTAAAGACACATGTGTCTTCGTCAAAGATA 180
Dd	482 CCAATCAGATAGTCTCCTGTCTCGAATATAGAGCTTAGACACATGTGTCTTCGTCAAAGATA 541
Qy	181 CATGTCTTCAGATTTTTTTTATCATTTCACCCCCTAGACACACTCTTAAGACACAACCTTAAGAC 240

Job time : 4131 secs

Db 542 CAGTCTTGAGATTTTATCATTCATCCCTAGACACACTCTTAAGACACAACTTAAGAC 601
QY 241 ACCATTGTACATGCCCTAAC 261
Db 602 ACCCACTGTGCATGCCCTTAC 622

RESULT 15
CC397966/c
LOCUS
DEFINITION CC397966 769 bp DNA linear GSS 19-MAY-2003
genomic survey sequence.
ACCESSION CC397966
VERSION CC397966.1 GI:30878056
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 769)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
Maize Genomics Consortium
Unpublished (2003)
JOURNAL
COMMENT Other_GSSs: PUHDC37TD
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.

FEATURES
source
1..769
/organism="Zea mays"
/mol_type="genomic DNA"
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/db_xref="taxon:4577"
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Cor selected genomic DNA library"

ORIGIN
Query Match 30.2%; Score 248.2; DB 9; Length 769;
Best Local Similarity 96.9%; Pred. No. 2.5e-62;
Matches 253; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 CTGCACGGTACTCCAAGTATTAAGACACAGCTAAACACAACTAATGCGTGGTCAATGTC 60
Db 459 CTGCACGGTACTCCAAGTATTAAGACACAGCTAAACACAACTAATGCGTGGTCAATGTC 400
QY 61 TAAACATGTGCTTACCATTATTCATTGTCATCAATCAGAACATTCATTAATTAAGTGA 120
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QY 121 CCAATCAGATAGTCTCCTCGCGATATAGAGCTAAGACACTGTGTCCTTCGTCAGATA 180
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QY 181 CATGCTTTCAGATTTTTCATTTCACCCCTAGACACACTCTTAAGACACAACTTAAGAC 240
Db 279 CATGCTTTCAGATTTTTCATTTCACCCCTAGACACACTCTTAAGACACAACTTAAGAC 220
QY 241 ACCATTGTACATGCCCTAAC 261
Db 219 ACCCACTGTGCATGCCCTTAC 199

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.
OM nucleic - nucleic search, using sw model
Run on: March 5, 2006, 09:29:49 ; Search time 620 Seconds
(without alignments)
8846.842 Million cell updates/sec
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Perfect score: 823
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Minimum DB seq length: 0
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6: Geneseqn2002s.*
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8: Geneseqn2003s.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004s.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	823	100.0	823	6	Aas96569 Corn prom
2	564	68.5	1587	6	Aas96566 Corn prom
C 3	231	28.1	1578	13	Adx48086 Plant ful
4	227	27.6	6343	3	Aas57891 Maize glo
5	220.2	26.8	1326	13	Adx60974 Plant ful
6	209.2	25.4	6550	2	Aav63717 Maize per
7	209.2	25.4	9299	2	Aav63730 Vector pl
8	209.2	25.4	9408	2	Aav63731 Vector pl
C 9	179.4	21.8	485	13	Adx49209 Plant ful
10	123.2	15.0	1088	13	Adt17641 Plant cdn
11	110.2	13.4	720	6	Aal37816 Corn KCP-
12	99.2	12.1	737	13	Adx53136 Plant ful
13	74.6	9.1	769	3	Aac43750 Zea mays
14	62	7.5	821	13	Adx33652 Plant ful
15	60	7.3	1696	13	Adx61698 Plant ful
16	59	7.2	791	13	Adx30094 Plant ful
17	59	7.2	795	13	Adx30071 Plant ful
18	56.8	6.9	765	13	Adx31426 Plant ful
19	53.6	6.5	1090	13	Adx50035 Plant ful

C	20	53.6	6.5	1318	13	ADO83463	Ado83463 Plant ful
C	21	50.6	6.1	505	13	ADX33788	Adx33788 Plant ful
C	22	50.6	6.1	2074	13	ADX52602	Adx52602 Plant ful
C	23	49	6.0	781	13	ADX33856	Adx33856 Plant ful
C	24	47.6	5.8	1412	13	ADX46949	Adx46949 Plant ful
C	25	44.6	5.4	110000	12	ADQ97047_1	Continuation (2 of
C	26	44.2	5.4	1027	13	ADO83991	Ado83991 Plant ful
C	27	44.2	5.4	1512	13	ADX52319	Adx52319 Plant ful
C	28	44.2	5.4	1538	13	ADX48874	Adx48874 Plant ful
C	29	43.4	5.3	271	12	ADQ04600	Adq04600 Maize hom
C	30	43.4	5.3	377	13	ADX10043	Adx10043 Plant ful
C	31	43.4	5.3	891	13	ADX34170	Adx34170 Plant ful
C	32	43.4	5.3	1184	13	ADX35171	Adx35171 Plant ful
C	33	43.4	5.3	1272	13	ADO83107	Ado83107 Plant ful
C	34	43.4	5.3	1676	13	ADX62396	Adx62396 Plant ful
C	35	43.4	5.3	1696	12	ADM47884	Adm47884 Polynucle
C	36	43.4	5.3	1699	13	ADX60046	Adx60046 Plant ful
C	37	43.4	5.3	1707	13	ADX63325	Adx63325 Plant ful
C	38	43.4	5.3	1807	13	ADX62639	Adx62639 Plant ful
C	39	43.4	5.3	2000	8	ADA71938	Ada71938 Rice gene
C	40	43.4	5.3	2025	3	AAC51726	Aac51726 Zea mays
C	41	43.4	5.3	2109	13	ADX64747	Adx64747 Plant ful
C	42	42.2	5.1	527	13	ADX29247	Adx29247 Plant ful
C	43	41.8	5.1	264	12	ADQ04637	Adq04637 Maize hom
C	44	41.8	5.1	281	12	ADQ04636	Adq04636 Maize hom
C	45	41.8	5.1	398	13	ADX12232	Adx12232 Plant ful

ALIGNMENTS

RESULT 1
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ID AAS96569 standard; DNA; 823 BP.

XX AAS96569;
AC AAS96569;
DT 26-FEB-2002 (first entry)
XX
DE Corn promoter sequence #12.
XX
KW Corn; male reproductive tissue; plant regulatory sequence; Zea mays;
KW promoter; transcription regulation; operably linked gene; monocot; dicot;
KW wheat anther; plant fertility; insect tolerance; pathogen tolerance;
KW herbicide tolerance; ds.
XX
OS Zea mays.
XX
PN WO200183790-A2.
XX
PD 08-NOV-2001.
XX
PF 30-APR-2001; 2001WO-US013739.
XX
PR 01-MAY-2000; 2000US-0201255P.
XX (MONS) MONSANTO TECHNOLOGY LLC.
XX
PI Conner TW, Dubois P, Malven M, Masucci JD;
WPI; 2002-055481/07.
XX
PT Novel promoters isolated from corn for controlling gene expression in
PT male reproductive tissues, such as anthers, tassels, and to regulate
PT transcription of target genes including genes for insect or pathogen
XX tolerance.
PS Claim 1; Page 113-114; 121pp; English.
XX
CC The present invention relates to the isolation of plant regulatory
CC sequences from the male reproductive tissues of corn (Zea mays). The
CC promoter sequences, fragments, regions or cis elements of the sequences,
CC are capable of regulating transcription of an operably linked DNA

CC sequence. The promoter sequences confer enhanced expression of operably
CC linked genes in monocot or dicot male reproductive tissues, such as
CC anthers, especially wheat anthers and is useful for regulating
CC transcription of a DNA sequence, by operably linking the DNA sequence to
CC the promoter. The promoter sequences are useful in plants to regulate
CC transcription of target genes including genes for control of fertility,
CC insect or pathogen tolerance and herbicide tolerance. They are also
CC useful as probes or primers in nucleic acid hybridisation experiments.
CC The promoter sequences can be used in hybridisation assays of other plant
CC tissues to identify closely related or homologous genes and associated
CC regulatory sequences. AAS96558-AAS96577 represent the corn promoter
CC sequences of the present invention
XX
SQ Sequence 823 BP; 244 A; 209 C; 161 G; 209 T; 0 U; 0 Other;
Query Match 100.0%; Score 823; DB 6; Length 823;
Best Local Similarity 100.0%; Pred. No. 9.9e-256;
Matches 823; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db |||||
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Db |||||
Qy 61 TAAACATGTGCTTACCATTATTCATTATCAATCAGAACATTCATTAATTAAGTGA 120
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Db |||||
Qy 121 CCAATCAGATAGTCTCTGTCCTCCGAATATAGAGTAAAGACACTGTGCTTCGTAAGATA 180
Db |||||
Qy 181 CATGCTTGAGATTTTACATTCACCCCTAGACACACTCTAAGACACAACTTAAGAC 240
Db |||||
Qy 181 CATGCTTGAGATTTTACATTCACCCCTAGACACACTCTAAGACACAACTTAAGAC 240
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Db |||||
Qy 241 ACCAATGTACATGCCCTAACTGGCAGCGCTACGTAGGGGTATTCAAGAACCAACCATG 300
Db |||||
Qy 301 TACAGTTGTCAGAGTGAATGGTATTGCTTCAGATTAAGCTAATTTAGACTGA 360
Db |||||
Qy 301 TACAGTTGTCAGAGTGAATGGTATTGCTTCAGATTAAGCTAATTTAGACTGA 360
Db |||||
Qy 361 TGCAGCTCAATTCATAGACACAAACAGTGTAGAGCCGTATAAGCAATTAAGCAACA 420
Db |||||
Qy 361 TGCAGCTCAATTCATAGACACAAACAGTGTAGAGCCGTATAAGCAATTAAGCAACA 420
Db |||||
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Db |||||
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Qy 781 GATCTCTCTCCCTCTCCCTCTCCGATCCATTTCTCCAGCGCAG 823
Db |||||

Db 781 GATCTCTCTCCCTCTCCCTCTCCGATCCATTTCTCCAGCGCAG 823
RESULT 2
AAS96566
ID AAS96566 standard; DNA; 1587 BP.
XX AAS96566
AC AAS96566
XX
DT 26-FEB-2002 (first entry)
XX
DE Corn promoter sequence #9.
XX
KW Corn; male reproductive tissue; plant regulatory sequence; Zea mays;
KW promoter; transcription regulation; operably linked gene; monocot; dicot;
KW wheat anther; plant fertility; insect tolerance; pathogen tolerance;
KW herbicide tolerance; ds.
XX
OS Zea mays.
XX
PN W0200183790-A2.
XX
PD 08-NOV-2001.
XX
PF 30-APR-2001; 2001WO-US013739.
XX
PR 01-MAY-2000; 2000US-0201255P.
XX
PA (MONS) MONSANTO TECHNOLOGY LLC.
XX
PI Conner TW, Dubois P, Malven M, Masucci JD;
XX
XX MPI; 2002-055481/07.
XX
PT Novel promoters isolated from corn for controlling gene expression in
PT male reproductive tissues, such as anthers, tassels, and to regulate
PT transcription of target genes including genes for insect or pathogen
PT tolerance.
XX
PS Claim 1; Page 111-112; 121pp; English.
XX
CC The present invention relates to the isolation of plant regulatory
CC sequences from the male reproductive tissues of corn (Zea mays). The
CC promoter sequences, fragments, regions or cis elements of the sequences,
CC are capable of regulating transcription of an operably linked DNA
CC sequence. The promoter sequences confer enhanced expression of operably
CC linked genes in monocot or dicot male reproductive tissues, such as
CC anthers, especially wheat anthers and is useful for regulating
CC transcription of a DNA sequence, by operably linking the DNA sequence to
CC the promoter. The promoter sequences are useful in plants to regulate
CC transcription of target genes including genes for control of fertility,
CC insect or pathogen tolerance and herbicide tolerance. They are also
CC useful as probes or primers in nucleic acid hybridisation experiments.
CC The promoter sequences can be used in hybridisation assays of other plant
CC tissues to identify closely related or homologous genes and associated
CC regulatory sequences. AAS96558-AAS96577 represent the corn promoter
CC sequences of the present invention
XX
SQ Sequence 1587 BP; 435 A; 385 C; 375 G; 392 T; 0 U; 0 Other;
Query Match 68.5%; Score 564; DB 6; Length 1587;
Best Local Similarity 99.1%; Pred. No. 1.5e-171;
Matches 567; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 252 ATGCCCTAACTGGCAGCCGCTACGTAGGGCTATTCAAGAACCAACCAATGTACAGTTGTTG 311
Db |||||
Qy 992 ATGCCCTAACTGGCAGCCGCTACGTAGGGCTATTCAAGAACCAACCAATGTACAGTTGTTG 1051
Db |||||
Qy 312 CAACGTGAATGGTTATTGCTTTCAGATTAAAGCTAATTTATTAGACTGATGAGTGCAG 371
Db |||||
Qy 1052 CAACGTGAATGGTTATTGCTTTCAGATTAAAGCCAAATGTTTAGCTGATGACCTGCA 1111
Db |||||
Qy 372 TTCATAGAGACAAACAGTGTAGAACCCGTATAGCATTAAGCAAAACAGCGAATTTG 431
Db |||||

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Qy	432	CTTAGCTACAAACCAATTGCTGGGCTTCATGGGCATCGCAGAAAGTATTGTGGCTGCATA	491
Db	1172	CTTAGCTACAAACCAATTGCTGGGCTTCATGGGCATCGCAGAAAGTATTGTGGCTGCATA	1231
Qy	492	TTGCTGAAATTTATACGAGGAGGCCCAAGGCCCATCACTTCACTTCGAGGTACAGCAATTGTAC	551
Db	1232	TTGCTGAAATTTATACGAGGAGGCCCAAGGCCCATCACTTCACTTCGAGGTACAGCAATTGTAC	1291
Qy	552	TTTTTGTTAAAGTCTCGATAAATTTGTTCACTTAAATAGACCAGTTCAATTCTGGTTCTA	611
Db	1292	TTTTTGTTAAAGTCTCGATAAATTTGTTCACTTAAATAGACCAGTTCAATTCTGGTTCTA	1351
Qy	612	GTCAACATGCTCGATCCACGGGGAGCGAGGACGAATGTGTGGCCCGCCGACGTGAG	671
Db	1352	GTCAACATGCTCGATCCACGGGGAGCGAGGACGAATGTGTGGCCCGCCGACGTGAG	1411
Qy	672	GCCAAGCCGAGCCGGTCTGTCGGTCCAAACACACCCCTCGTTTACTATATATACACAGA	731
Db	1412	GCCAAGCCGAGCCGGTCTGTCGGTCCAAACACACCCCTCGTTTACTATATATACACAGA	1471
Qy	732	CGCACGATACCCATATCGTGGTGTGAAGCACTGAAAAACAGCCGAGCGATCTCCTCTC	791
Db	1472	CGCACGATACCCATATCGTGGTGTGAAGCACTGAAAAACAGCCGAGCGATCTCCTCTC	1531
Qy	792	CCTCTCCTCTCCGATCCATTTCTCCAGGGGAG	823
Db	1532	CCTCTCCTCTCCGATCCATTTCTCCAGGGGAG	1563

RESULT 3

RESULT 3
ADX48086/C

ADX48086/C
ID ADX48086 standard; cDNA: 1578 BP.

AC ADX48086:

XX DT 21-APR-2005 (first entry)

Plant full length insert polynucleotide seqid 22826.

plant protectant; plant growth regulant; gene therapy; plant;
recombinant DNA construct; physical array; plant breeding marker;
cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
extreme osmotic condition; pathogen tolerance; pest tolerance;
growth rate; cell cycle pathway; disease resistance;
galactomannan production; lignin production; plant growth regulator;
yield; plant growth; plant development; seed oil; protein yield;
protein content; gene; ss.

OS Unidentified.

XX
PN
US2004034888-A1.

XX
PD
19-FEB-2004XX
PF 28-APR-2003: 2003US-00425114.

XX
PP
06-MAY-1999. 0917S-00304517

PR 05-NOV-2001; 2001US-00985678.
XX

PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.

PA	(ZHOU/)	ZHOU Y
PA	(ZHOU/)	ZHOU Y

PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E

PA (SCRE/) SCREEN S E.
PA : (TABA/) TABASKA J E

PA : (TABA/) TABASKA J E.
PA (CAOV/) CAO Y

PA (CAOY//) CAO Y.
XX

XX
PI
Liu J. Zhou Y. Kovalic DK. Screen SE. Tabaska JE. Cao Y:

XX
DB WPT: 2004-180133/17

XX DR

PT New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.

PS Claim 1; SEQ ID NO 22826; 15pp; English.

The invention describes a recombinant DNA construct comprising a polynucleotide consisting of a sequence encoding an amino acid sequence available in electronic form from the US patent office at ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one or stress condition or for modifying seed oil or protein yield and/or content. This sequence represents a plant full length insert polynucleotide that can be used in the recombinant DNA construct of the invention.

Sequence 1578 BP: 380 A: 391 C: 429 G: 378 T: 0 U: 0 Other: 0

Query Match	28.1%	Score 231	DB 13	Length 1578
Best Local Similarity	92.4%	Pred. No. 1.5e-63		
Matches 243	Conservative	0	Mismatches 20	Indels 0
		0		Caps 0

Qy	2	TCGACGGTACTCGAAGTATAAGACACACAGCTAAACACACACATTAATCGAGTGGTCAATGTCT	61
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Db	994	AAAAACATGTGTCTTACCATATTAATTGTACCAATCAGAGCATTCATTAATAATTAAGGTGAC	935
Qy	122	CAATCAGATAGTCTCTGTCGCCGAATATAGAGGTAAGACACTGTGTCTTCGTCGAAGATAC	181
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Qy	182	ATGTCCTTGAGATTTTTTTCATTCACCCGCCCTAGACACACTCTTAAGACACAACTTAAAGACA	241
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Qy	242	CCCATTTGTACATGCCCTAACTGG	264
Db	814	CCCACTGTACATGCCCTAACTGG	792

RESULT 4

RESUL 4
AAA57891

AAA57891
ID AAA57891 standard; DNA: 6343 BP.

XX
AC AAA57891:XX
DT 10-OCT-2000 (first entry)

XX DE Maize storage (α) gene

XX Maize; glossy2; gl2; cuticle; cuticular lipid biosynthesis;
KW lipid composition; lipid quantity; disease resistance; pest resistance;
KW wind resistance; frost resistance; UV resistance; transgenic plant;
KW antisense inhibition; ds.

XX
05 Zea mays.XX
PN
TTS6060644-AXX
RD
09-MAY-2000

Db 254 CCTATCAGCTAGTCTCTGCTCCAAACATAGACATTGCTGCTCAAGTA 313
Oy 181 CATGCTTGAGATTTTACATTCACCCCTAGACACACTCTTAAGACAACTTAAGAC 240
Db 314 CATGCTTGAGATTTTACATTCACCCCTAGACACACTCTTAAGACAACTTAAGAC 372
Oy 241 ACCCATGTATCATGCCCTTAACCTGGACCG 269
Db 373 ACATATTGTATCATGCCCTTAAGGGAGATCG 401

RESULT 6
AAV63717
ID AAV63717 standard; DNA; 6550 BP.
XX AAV63717;
XX
XX 12-APR-1999 (first entry)
XX
DE Maize per5 root preferential cationic peroxidase gene.
XX Peroxidase; per5 gene; maize; corn; transgenic plant; promoter; root; ds.
XX
XX Zea mays.
XX
XX Key Location/Qualifiers
FT promoter 1. .4215
FT /tag= a
FT /note= "this region is specifically claimed in Claim 1"
FT misc_feature 1. .4200
FT /tag= c
FT /note= "this region is specifically claimed in Claim 1"
FT misc_feature 1. .4148
FT /tag= b
FT /note= "this region is specifically claimed in Claim 1"
FT misc_feature 2532. .4215
FT /tag= f
FT /note= "this region is specifically claimed in Claim 1"
FT misc_feature 2532. .4200
FT /tag= e
FT /note= "this region is specifically claimed in Claim 1"
FT misc_feature 2532. .4148
FT /tag= d
FT /note= "this region is specifically claimed in Claim 1"
FT misc_feature 3187. .4215
FT /tag= i
FT /note= "this region is specifically claimed in Claim 1"
FT misc_feature 3187. .4200
FT /tag= h
FT /note= "this region is specifically claimed in Claim 1"
FT misc_feature 3187. .4148
FT /tag= g
FT /note= "this region is specifically claimed in Claim 1"
FT misc_feature 4086. .4215
FT /tag= l
FT /note= "this region is specifically claimed in Claim 1"
FT misc_feature 4086. .4200
FT /tag= k
FT /note= "this region is specifically claimed in Claim 1"
FT misc_feature 4086. .4148
FT /tag= j
FT /note= "this region is specifically claimed in Claim 1"
FT CDS 4201. .6068
FT /tag= m
FT /product= "peroxidase"
FT /note= "contains introns"
FT exon 4201. .4425
FT /tag= n
FT /number= 1
FT misc_feature 4420. .5064
FT /tag= o
FT /note= "this sequence is specifically claimed in Claim 2"

FT intron 4426. .5058
FT /tag= p
FT /number= 1
FT /note= "this intron is specifically claimed in Claim 2"
FT exon 5059. .5250
FT /tag= q
FT /number= 2
FT misc_feature 5245. .5388
FT /tag= r
FT /note= "this sequence is specifically claimed in Claim 2"
FT intron 5251. .5382
FT /tag= s
FT /number= 2
FT /note= "this intron is specifically claimed in Claim 2"
FT exon 5383. .5548
FT /tag= t
FT misc_feature 5542. .5654
FT /tag= u
FT /note= "this sequence is specifically claimed in Claim 2"
FT misc_feature 5542. .5654
FT /tag= x
FT /note= "this sequence is specifically claimed in Claim 2"
FT intron 5549. .5649
FT /tag= v
FT /number= 3
FT /note= "this intron is specifically claimed in Claim 2"
FT exon 5650. .6065
FT /tag= w
FT /number= 4
FT 3'UTR 6068. .6431
FT /tag= y
FT /note= "transcription termination sequence, specifically claimed in Claim 3"
FT
FT
XX WO9856921-A1.
XX
XX 17-DEC-1998.
XX
XX 10-JUN-1998; 98WO-US011921.
XX
XX 12-JUN-1997; 97US-0049752P.
XX
XX (DOWC) DOW AGROSCIENCES-LLC.
XX
XX Ainley M, Armstrong K, Belmar S, Folkerts O, Hopkins N, Menke MA,
XX Paredy D, Petolino JF, Smith K, Woosley A;
XX WPI; 1999-080904/07.
XX P-PSDB; AAW87893.
XX
XX New isolated regulatory sequences for transgenic plants - which are
XX derived from the maize root preferential cationic peroxidase protein
XX (per5) gene.
XX
XX Claim 1; Page 84-89; 150pp; English.
XX
XX This is the nucleotide sequence of the maize per5 root preferential
XX cationic peroxidase gene, which encodes a 333-amino acid peroxidase
XX polypeptide (see AAW87893). Genomic clones comprising per5 sequences were
XX isolated from a maize W22 genomic library using a probe based on isolated
XX per5 cDNA. Overlapping subfragments of the gene were sequenced to
XX determine the complete 5550 bp sequence of the per5 gene. Regulatory
XX sequences derived from the per5 gene, including the promoter, introns and
XX 3' untranslated region (3'UTR), are used in claimed recombinant gene
XX cassettes for controlling expression of recombinant genes in selected
XX tissue, especially the root, of transformed plants, particularly maize.
XX The gene cassettes can be used for expression of heterologous genes such
XX as those that confer tolerance to herbicides, insects or viruses, and
XX genes that provide improved nutritional value or processing
XX characteristics to the plant. Use of the per5 3'UTR sequences provides
XX enhanced expression compared to similar gene cassettes utilising the nos
XX 3'UTR

```
XX SQ Sequence 6550 BP; 1844 A; 1427 C; 1346 G; 1933 T; 0 U; 0 Other;
Query Match 25.4%; Score 209.2; DB 2; Length 6550;
Best Local Similarity 90.1%; Pred. No. 4e-56;
Matches 236; Conservative 0; Mismatches 23; Indels 3; Gaps 1;

Qy 2 TGCACGGTACTCCAGTATAGACACAGCTAAACACACACATATG---CAGTGGTCATG 58
Db 1355 TGCACAGTACTCCAGTATAGACACACACTAAACACACACATATATACAGTGGTTATA 1414

Qy 59 TCTAAACATGCTGCTTACCATATTCATTGTATCAATCAGAACATTCATTAATAAATTAAGT 118
Db 1415 TCTAAACATGCTGCTTACCATATTCATTGTATCAATCAGAACATTCATTAATAAATTAAGT 1474

Qy 119 GACCAATCAGATAGTCTCTCTCCGAATATAGAGCTAAAGACATGCTGTCTTCGTCAAGA 178
Db 1475 GACCAATCAGCTAGCTCTCTCTCGAACATAGAGCTAAGACATGCTGTCTTCGTCAAGA 1534

Qy 179 TACATGCTTGAGATTTTTCATATTCACCTCCCTAGACACACTCTAAGACACAACTTAAG 238
Db 1535 TACATGCTTGAGATTTTTCATATTCACCTCCCTAGACACACTCTAAGACACAACTTAAG 1594

Qy 239 ACACCATTTGACATGCCCTAA 260
Db 1595 ACACCATTTGACATGCTCTTA 1616

RESULT 7
AAV63730
ID AAV63730 standard; DNA; 9299 BP.
XX AC AAV63730;
XX DT 12-APR-1999 (first entry)
XX DE Vector plasmid PerGUS16.
XX KW Peroxidase; per5 gene; maize; corn; transgenic plant; promoter; root;
XX KW vector; plasmid PerGUS16; beta-glucuronidase; uidA; reporter gene; ds;
XX KW circular; cyclic.
XX OS Escherichia coli.
XX OS Zea mays.
XX OS Agrobacterium tumefaciens.
XX OS Synthetic.
XX OS Chimeric.
XX FH Key Location/Qualifiers
FT Promoter 48..4247
FT FT /*tag= a
FT FT /note= "per5 promoter and untranslated leader"
FT FT exon 4248..4263
FT FT /*tag= b
FT FT /note= "per5 exon 1"
FT FT CDS 4264..6068
FT FT /*tag= c
FT FT /product= "beta-glucuronidase"
FT FT /note= "Escherichia coli uidA reporter gene"
FT FT 3' UTR 6069..6111
FT FT /*tag= d
FT FT /note= "3' untranslated region from pBI221"
FT FT 3' UTR 6122..6396
FT FT /*tag= e
FT FT /note= "nos 3'UTR"
FT FT misc_feature 6397..6407
FT FT /*tag= f
FT FT /note= "linker"
FT FT 6408..9299
FT FT misc_feature
FT FT /*tag= g
FT FT /note= "Bluescript II SK-"
XX PN W09B56921-A1.
```

```
XX PD 17-DEC-1998.
XX PF 10-JUN-1998; 98WO-US011921.
XX PR 12-JUN-1997; 97US-0049752P.
XX PA (DOWC) DOW AGROSCIENCES LLC.
XX PI Ainley M, Armstrong K, Belmar S, Folkerts O, Hopkins N, Menke MA,
PI Pareddy D, Petolino JF, Smith K, Woosley A;
XX DR WPI; 1999-080904/07.
XX PT New isolated regulatory sequences for transgenic plants - which are
XX PT derived from the maize root preferential cationic peroxidase protein
XX PT (per5) gene.
XX PS Example 11; Page 108-112; 150pp; English.
XX CC This is the nucleotide sequence of PerGUS, a plasmid containing 4 kb of
XX CC the maize root preferential cationic peroxidase per5 gene comprising the
XX CC per5 promoter, untranslated leader, and the first 5 codons of the coding
XX CC region (i.e., nucleotides 1-4200 of the sequence given in AAV63717), as
XX CC well as the GUS gene, and the nos 3' untranslated region (3'UTR). It does
XX CC not include an intron in the untranslated region. The invention relates
XX CC to new isolated regulatory sequences, especially promoter, intron and
XX CC 3'UTR sequences, of the maize per5 gene. Claimed recombinant gene
XX CC cassettes comprising per5 regulatory sequences are used to control
XX CC expression of recombinant genes in selected tissue, especially the root,
XX CC of transformed plants, particularly maize
XX SQ Sequence 9299 BP; 2573 A; 2114 C; 2158 G; 2453 T; 0 U; 1 Other;

Query Match 25.4%; Score 209.2; DB 2; Length 9299;
Best Local Similarity 90.1%; Pred. No. 4.8e-56;
Matches 236; Conservative 0; Mismatches 23; Indels 3; Gaps 1;

Qy 2 TGCACGGTACTCCAGTATAGACACAGCTAAACACACAACTAATG---CAGTGGTCATG 58
Db 1402 TGCACAGTACTCCAGTATAGACACACACTAAACACACAACTAATATACAGTGGTTATA 1461

Qy 59 TCTAAACATGCTGCTTACCATATTCATTGTATCAATCAGAACATTCATTAATAAATTAAGT 118
Db 1462 TCTAAACATGCTGCTTACCATATTCATTGTATCAATCAGAACATTCATTAATAAATTAAGT 1521

Qy 119 GACCAATCAGATAGTCTCTCTCCGAATATAGAGCTAAGACACTGTGCTTCGTCAAGA 178
Db 1522 GACCAATCAGCTAGCTCTCTCTCGAACATAGAGCTAAGACACTGTGCTTCGTCAAGA 1581

Qy 179 TACATGCTTGAGATTTTTCATATTCACCTCCCTAGACACACTCTAAGACACAACTTAAG 238
Db 1582 TACATGCTTGAGATTTTTCATATTCACCTCCCTAGACACACTCTAAGACACAACTTAAG 1641

Qy 239 ACACCATTTGACATGCCCTAA 260
Db 1642 ACACCATTTGACATGCTCTTA 1663

RESULT 8
AAV63731
ID AAV63731 standard; DNA; 9408 BP.
XX AC AAV63731;
XX DT 12-APR-1999 (first entry)
XX DE Vector plasmid PERGUSPER3.
XX KW Peroxidase; per5 gene; maize; corn; transgenic plant; promoter; root;
XX KW vector; plasmid PERGUSPER3; beta-glucuronidase; uidA; reporter gene; ds;
XX KW circular; cyclic.
XX PN W09B56921-A1.
```

OS Escherichia coli.
OS Zea mays.
OS Agrobacterium tumefaciens.
OS Synthetic.
OS Chimeric.
XX

FH Key Location/Qualifiers
FT misc_feature 1..42
FT /tag= a
FT /note= "polylinker site"
FT misc_feature 43..53
FT /tag= b
FT /note= "synthetic linker"
FT promoter 54..4253
FT /tag= c
FT /note= "per5 promoter and untranslated leader"
FT exon 4254..4269
FT /tag= d
FT /note= "per5 exon 1"
FT CDS 4266..6074
FT /tag= e
FT /product= "beta-glucuronidase"
FT /note= "Escherichia coli uidA reporter gene"
FT 3'UTR 6075..7117
FT /tag= f
FT 3'UTR 6140..6510
FT /tag= g
FT /note= "per5 3'UTR"
FT misc_feature 6517..8408
FT /tag= h
FT /note= "Bluescript II SK-"
XX

PN W09856921-A1.
XX
XX 17-DEC-1998.
XX
XX 10-JUN-1998; 98WO-US011921.
XX
XX 12-JUN-1997; 97US-0049752P.
XX
XX (DOWC) DOW AGROSCIENCES LLC.
XX
XX Ainley M, Armstrong K, Belmar S, Folkerts O, Hopkins N, Menke MA;
XX Paredy D, Petolino JF, Smith K, Woosley A;
XX WPI; 1999-080904/07.
XX
XX New isolated regulatory sequences for transgenic plants - which are
XX derived from the maize root preferential cationic peroxidase protein
XX (per5) gene.
XX
XX Example 12; Page 113-117; 150pp; English.
XX
XX This is the nucleotide sequence of PERGUSPER3, a plasmid containing 4.2
XX kb of the maize root preferential cationic peroxidase per5 gene
XX comprising the per5 promoter, untranslated leader, and the first 5 codons
XX of the coding region (i.e. nucleotides 1-4200 of the sequence given in
XX AAV63717), as well as the GUS gene, and the per5 3' untranslated region
XX (3'UTR, i.e. nucleotides 6069-6439 of the sequence given in AAV63717). It
XX does not include an intron in the untranslated region. Experiments
XX demonstrated that the per5 promoter, in the absence of an intron, drives
XX constitutive expression of transgenes in rice. The invention relates to
XX new isolated regulatory sequences, especially promoter, intron and 3'UTR.
XX sequences, of the maize per5 gene. Claimed recombinant gene cassettes
XX comprising per5 regulatory sequences are used to control expression of
XX recombinant genes in selected tissue, especially the root, of transformed
XX plants, particularly maize
XX

SQ Sequence 9408 BP; 2591 A; 2138 C; 2178 G; 2500 T; 0 U; 1 Other;
Query Match 25.4%; Score 209.2; DB 2; Length 9408;
Best Local Similarity 90.1%; Pred. No. 4.9e-56;

Matches 236; Conservative 0; Mismatches 23; Indels 3; Gaps 1;
Qy 2 TGCACGGTACTCCAGTATTAAGACACAGCTAAACACACATAATG---CAGTGGTCATG 58
Db 1408 TGCACAGTACTCCCAAGTATTAAGACACAACTAAACACACATAATAATACAGTGGTTATA 1467
Qy 59 TCTAAACATGTGTCTTACCATTATTCATTGTATCAATCAGAACATTCATTAATAAATTAAGT 118
Db 1468 TCTAAACATGTGTCTTACCATTATTCATTGTATCAATCAGAACATTCATTAATAAATTAAGT 1527
Qy 119 GACCAATCAGATAGTCTCTGTCGCCGAATATAGAGCTAAGACACTGTCTTCTGTCGAAGA 178
Db 1528 GACCAATCAGCTAGCTCTCTGTCGCCGAATATAGAGCTAAGACACTGTCTTCTGTCGAAGA 1587
Qy 179 TACATGCTCTGAGATTTTATACATTACCCCTCCCTCCCAAGACACACTCTAAGACACACTTAAG 238
Db 1588 TACATGCTCTGAGTATTTTATACATTACCCCTCCCTCCCAAGACACACTCTAAGACACACTTAAG 238
Qy 239 ACACCCATTGTACATGCCCTAA 260
Db 1648 ACACCCATTGTACATGCCCTTA 1669

*RESULT 9
ADX49209/c
ID ADX49209 standard; cDNA; 485 BP.
XX AC ADX49209;
XX
XX 21-APR-2005 (first entry)
XX
XX Plant full length insert polynucleotide seqid 23949.
XX
XX plant protectant; plant growth regulant; gene therapy; plant;
XX recombinant DNA construct; physical array; plant breeding marker;
XX cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
XX extreme osmotic condition; pathogen tolerance; pest tolerance;
XX growth rate; cell cycle pathway; disease resistance;
XX galactomannan production; lignin production; plant growth regulator;
XX yield; plant growth; plant development; seed oil; protein yield;
XX protein content; gene; ss.
XX
XX Unidentified.
XX
XX US2004034888-A1.
XX
XX 19-FEB-2004.
XX
XX 28-APR-2003; 2003US-00425114.
XX
XX 06-MAY-1999; 99US-00304517.
XX
XX 05-NOV-2001; 2001US-00985678.
XX
XX (LIUJ/) LIU J.
XX (ZHOU/) ZHOU Y.
XX (KOVA/) KOVALIC D K.
XX (SCRE/) SCREEN S E.
XX (TABA/) TABASKA J E.
XX (CAOY/) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX pests, for conferring increased resistance to plant disease, or for
XX improving yield.
XX
XX Claim 1; SEQ ID NO 23949; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence.

CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID=2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.

XX SQ Sequence 485 BP; 120 A; 126 C; 129 G; 110 T; 0 U; 0 Other;

Query Match 21.8%; Score 179.4; DB 13; Length 485;
Best Local Similarity 94.4%; Pred. No. 4.3e-47;
Matches 186; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 64 AACATGTCCTTACCATATTCATTGTATCAATCAAGACATTCATTAATTAAGTGACCA 123
DB 481 AAAACATGTCCTTACCATATTCATTGTATCAATCAAGACATTCATTAATTAAGTGACCA 422
QY 124 ATCAGATAGTCCTTGTCCCGAATATAGAGCTTAAGACACTGTGTCCTCAAGATACAT 183
DB 421 ATCAGATAGTCCTTGTCCCGAATATAGAGCTTAAGACACTGTGTCCTCAAGATACGT 362
QY 184 GTCCTGAGATTTTACATTCACCCCTAGACACACTCTAAGACACAACTTAAGACACC 243
DB 361 GTCCTGAGATTTTACATTCACCCCTAGACACACTCTAAGACACAACTTAAGACACC 302
QY 244 CATTGTACATGCCCTAA 260
DB 301 CACTGTACATGCCCTTA 285

RESULT 10

ID ADT17641/c
ADT17641 standard; cDNA; 1088 BP.

XX AC ADT17641;

XX DT 13-JAN-2005 (first entry)

XX DE Plant cDNA, Seq ID 2967.

XX KW Plant; ss; gene; transgenic; cold tolerance; growth rate;
KW drought tolerance; disease resistance; galactomannan production;
KW plant growth regulator; heat tolerance; herbicide tolerance;
KW lignin production; extreme osmotic condition tolerance;
KW pathogens resistance; pest resistance; yield improvement; seed oil yield;
KW seed protein yield.

XX OS Viridiplantae.

XX PN US2004216190-A1.

XX PD 28-OCT-2004.

XX PF 18-DEC-2003; 2003US-00739930.

XX PR 28-APR-2003; 2003US-00424599.

XX PR 28-APR-2003; 2003US-00425115.

XX PA (KOVA/) KOVALIC D K.

XX PI Kovalic DK;

XX WP 2004-757369/74.

XX New recombinant DNA constructs useful in the field of biochemistry and
PT genetics, and in particular for producing transgenic plants with improved
PT biological characteristics.

XX Claim 1; SEQ ID NO 2967; 14pp; English.

XX The invention relates a recombinant DNA construct comprising a
XX polynucleotide having any of 5544 nucleotide sequences (cDNAs SEQ ID NO:
XX 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences
XX (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean,
XX Arabidopsis, wheat and rape but the specification does not indicate which
XX sequences is derived from which organism. Also included is a method of
XX producing a plant having an improved property, comprising transforming a
XX plant with a recombinant DNA construct comprising a promoter region
XX functional in a plant cell operably joined to a polynucleotide encoding a
XX polypeptide associated with the property, and growing the transformed a
XX plant. The property is selected from improving plant cold tolerance, for
XX manipulating growth rate in plant cells by modification of the cell cycle
XX pathway, for improving plant drought tolerance, for providing increased
XX resistance to plant disease, for galactomannan production, for production
XX of plant growth regulators, for improving plant heat tolerance, for
XX improving plant tolerance to herbicides, for increasing the rate of
XX homologous recombination in plants, for lignin production, for improving
XX plant tolerance to extreme osmotic conditions, for improving plant
XX tolerance to pathogens or pests, for yield improvement by modification of
XX photosynthesis, for modifying seed oil yield and/or content, for
XX modifying seed protein yield and/or content, for yield improvement by
XX modification of carbohydrate, nitrogen or phosphorus use and/or uptake
XX and for yield improvement by providing improved plant growth and
XX development under at least one stress condition. The polynucleotide may
XX also encode a plant transcription factor. The methods and compositions of
XX the present invention are useful in the field of biochemistry and
XX genetics, in particular for producing transgenic plants with improved
XX biological characteristics such as increased yield, improved plant
XX flow, increasing plant tolerance to cold or heat, improving plant
XX tolerance to extreme osmotic and drought conditions, and improving plant
XX tolerance to plant pests or pathogens. They can also be used in physical
XX arrays of molecules, plant breeding markers, computer-based storage and
XX analysis systems. The present sequence is one of the 5544 plant cDNA
XX sequences of the invention. Note: The sequence data for this patent did
XX not form part of the printed specification, but was obtained in
XX electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?DocID=20040216190.

XX Sequence 1088 BP; 265 A; 261 C; 260 G; 302 T; 0 U; 0 Other;

Query Match 15.0%; Score 123.2; DB 13; Length 1088;

Best Local Similarity 91.0%; Pred. No. 1.1e-28;

Matches 142; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

QY 105 CAATAAATTAAAGTGACCAATCAGATAGTCCTGTCCCGAATATAGAGCTAAGACACTG 164
DB 1088 CAATAAATTAAAGTGACCAATCAGATAGTCCTGTCCCGAATATAGAGCTAAGACACTG 1029
QY 165 TGTCTTCGTCAAGATACATGCTTTGAGATTTTATACATTCACCCCTTAGACACTCTA 224
DB 1028 TGTCTTCGTGTC-AGATACATGCTTTGAGATTTTATACATTCACCCCTTAGACACTCTA 970

QY 225 AGACACAACTTAAGACACCCCATTTGATGCGCTTAA 260

DB 969 AATCACAACTTAAGACACTCTATTGTATACATCCCTTA 934

RESULT 11

AAL37816

ID AAL37816 standard; DNA; 720 BP.

XX AC AAL37816;

XX DT 05-AUG-2002 (first entry)

XX DE Corn KCP-like protein encoding DNA, SEQ ID NO 8.

xx Antimicrobial; transgenic; plant; potato snakin antimicrobial protein;
KW GAS4; GAS45; GAST1 homologue; lysine- and cysteine- rich peptide;
KW KCP-like polypeptide; modulating; disease resistance; gene; ds.
XX
OS Zea mays.
XX
XX WO200222821-A2.
XX
XX 21-MAR-2002.
XX
XX 13-SEP-2001; 2001WO-US028429.
XX
XX 13-SEP-2000; 2000US-0232569P.
PR
PR 11-SEP-2001; 2001US-00950933.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Simmons CR, Navarro Acevedo PA;
PI
XX MPI; 2002-425842/45.
DR
DR P-PSDB; AAO21285.
XX
XX New polynucleotide encoding lysine- and cysteine-rich peptides-like
PT polypeptide useful for modulating the polypeptide level in a plant cell,
PT enhancing disease resistance.
XX
XX Claim 1; Page 118-119; 163pp; English.
XX
XX The invention relates to an isolated polynucleotide encoding a
CC polypeptide which is related to potato snakin antimicrobial protein and
CC GAS4 or GAS45 or GAST1 homologues, which is referred to as lysine- and
CC cysteine- rich peptides (KCP)-like polypeptide, having a nucleotide
CC sequence from 36 sequences of defined base pairs, given in the
CC specification. A recombinant expression cassette comprising the isolated
CC polynucleotide of the invention is useful for modulating the level of
CC (KCP)-like polypeptides in a plant cell, where the level of (KCP)-like
CC polypeptides is increased, and disease resistance is enhanced. This
CC polynucleotide sequence represents the DNA encoding a KCP-like protein of
CC the invention
XX
XX Sequence 720 BP; 195 A; 215 C; 163 G; 147 T; 0 U; 0 Other;
Query Match 13.4%; Score 110.2; DB 6; Length 720;
Best Local Similarity 90.1%; Pred. No. 1.5e-24;
Matches 118; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 1 CTGCACGGTACTCCAGTATAAGACACAGCTAAACACACACATATGCGTGTGTC 60
Db 578 CTGCACGGTACTCCAGTATAAGACACAGCTAAACACACACATATGCGTGTGTC 637
QY 61 TAAACATGTGCTTACCATATTCATTGATCAATCAGAACATTCATTAATAAAGTGA 120
Db 638 TAAACATGTGCTTACCATATTCATTGATCAATCAGAACATTCATTAATAAAGTGA 697
QY 121 CCAATCAGATA 131
Db 698 CCAAAAAA 708
RESULT 12
ADX53136
ID ADX53136 standard; cDNA; 737 BP.
XX
AC ADX53136;
XX
XX 21-APR-2005 (first entry)
XX
XX Plant full length insert polynucleotide seqid 27876.
XX
XX plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;

XX extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
XX protein content; gene; ss.
OS Unidentified.
XX
XX US2004034888-A1.
XX
XX 19-FEB-2004.
XX
XX 28-APR-2003; 2003US-00425114.
XX
XX 06-MAY-1999; 99US-00304517.
PR
PR 03-NOV-2001; 2001US-00985678.
XX
XX (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
PI
XX MPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
XX improving yield.
XX
XX Claim 1; SEQ ID NO 27876; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.upto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX
XX Sequence 737 BP; 182 A; 228 C; 174 G; 153 T; 0 U; 0 Other;
Query Match 12.1%; Score 99.2; DB 13; Length 737;
Best Local Similarity 92.1%; Pred. No. 5.6e-21;
Matches 116; Conservative 0; Mismatches 8; Indels 2; Gaps 1;
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Db 614 CTGCACGGTACTCCAGTATAAGACACAGCTAAACACACACATATGCGTGTGTC 671
QY 61 TAAACATGTGCTTACCATATTCATTGATCAATCAGAACATTCATTAATAAAGTGA 120
Db 672 TAAACATGTGCTTACCATATTCATTGATCAATCAGAACATTCATTAATAAAGTGA 731
QY 121 CCAATC 126
Db 732 CCAATC 737

ER

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PR 20-AUG-1999; 99US-0149929P;
PR 23-AUG-1999; 99US-0149902P;
PR 23-AUG-1999; 99US-0149930P;
PR 25-AUG-1999; 99US-0150566P;
PR 26-AUG-1999; 99US-0150884P;
PR 27-AUG-1999; 99US-0151065P;
PR 27-AUG-1999; 99US-0151066P;
PR 27-AUG-1999; 99US-0151080P;
PR 30-AUG-1999; 99US-0151303P;
PR 31-AUG-1999; 99US-0151438P;
PR 01-SEP-1999; 99US-0151930P;
PR 07-SEP-1999; 99US-0152363P;
PR 10-SEP-1999; 99US-0153070P;
PR 13-SEP-1999; 99US-0153758P;
PR 15-SEP-1999; 99US-0154018P;
PR 16-SEP-1999; 99US-0154033P;
PR 20-SEP-1999; 99US-0154779P;
PR 22-SEP-1999; 99US-0155139P;
PR 23-SEP-1999; 99US-0155486P;
PR 24-SEP-1999; 99US-0155659P;
PR 28-SEP-1999; 99US-0156458P;
PR 29-SEP-1999; 99US-0156598P;
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PR 05-OCT-1999; 99US-0157533P;
PR 06-OCT-1999; 99US-0157865P;
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PR 08-OCT-1999; 99US-0158232P;
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PR 14-OCT-1999; 99US-0159329P;
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PR 14-OCT-1999; 99US-0159331P;
PR 14-OCT-1999; 99US-0159637P;
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PR 18-OCT-1999; 99US-0159584P;
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PR 26-OCT-1999; 99US-0161360P;
PR 26-OCT-1999; 99US-0161361P;
PR 28-OCT-1999; 99US-0161920P;
PR 28-OCT-1999; 99US-0161922P;
PR 28-OCT-1999; 99US-0161933P;
PR 29-OCT-1999; 99US-0162142P;

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Best Local Similarity 98.7%; Pred. No. 5.4e-13;
Matches 74; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 809 CATTCTCCAGCGCAG 823
DB 61 CATTCTCCAGCGCAG 75

RESULT 14
ADX33652
ID ADX33652 standard; cDNA; 821 BP.
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```
XX ADX33652;
AC
XX 21-APR-2005 (first entry)
XX Plant full length insert polynucleotide seqid 16472.
XX plant protectant; plant growth regulant; gene therapy; plant;
XX recombinant DNA construct; physical array; plant breeding marker;
XX cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
XX extreme osmotic condition; pathogen tolerance; pest tolerance;
XX growth rate; cell cycle pathway; disease resistance;
XX galactomannan production; lignin production; plant growth regulator;
XX yield; plant growth; plant development; seed oil; protein yield;
XX protein content; gene; ss.
XX Unidentified.
XX OS
XX US2004034888-A1.
XX 19-FEB-2004.
XX 28-APR-2003; 2003US-00425114.
XX 06-MAY-1999; 99US-00304517.
XX 05-NOV-2001; 2001US-00985678.
XX (LIUJ/) LIU J.
XX (ZHOU/) ZHOU Y.
XX (KOVA/) KOVALIC D K.
XX (SCRE/) SCREEN S E.
XX (TABA/) TABASKA J E.
XX (CAOY/) CAO Y.
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX New recombinant DNA construct, useful for improving plant tolerance to
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX pests, for conferring increased resistance to plant disease, or for
XX improving yield.
XX Claim 1; SEQ ID NO 16472; 15pp; English.
XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence
XX available in electronic form from the US patent office at
XX ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
XX of the invention are also useful in physical arrays of molecules and as
XX plant breeding markers. The recombinant DNA construct is useful for
XX improving plant tolerance to cold, heat, drought, herbicides, extreme
XX osmotic conditions, pathogens or pests, for manipulating growth rate in
XX plant cells by modification of the cell cycle pathway, for conferring
XX increased resistance to plant disease, for producing galactomannan,
XX lignin or plant growth regulators, for increasing the rate of homologous
XX recombination in plants, for improving yield by modification of
XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
XX or by providing improved plant growth and development under at least one
XX stress condition or for modifying seed oil or protein yield and/or
XX content. This sequence represents a plant full length insert
XX polynucleotide that can be used in the recombinant DNA construct of the
XX invention.
XX SQ Sequence 821 BP; 187 A; 227 C; 214 G; 193 T; 0 U; 0 Other;
Query Match 7.5%; Score 62; DB 13; Length 821;
Best Local Similarity 100.0%; Pred. No. 6.9e-09;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	822 AG 823	
Db	61 AG 62	
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XX	ADX61698;	
XX	21-APR-2005 (first entry)	
XX	Plant full length insert polynucleotide seqid 32541.	
XX	plant protectant; plant growth regulant; gene therapy; plant;	
KW	recombinant DNA construct; physical array; plant breeding marker;	
KW	cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;	
KW	extreme osmotic condition; pathogen tolerance; pest tolerance;	
KW	growth rate; cell cycle pathway; disease resistance;	
KW	galactomannan production; lignin production; plant growth regulator;	
KW	yield; plant growth; plant development; seed oil; protein yield;	
KW	protein content; gene; ss.	
OS	Unidentified.	
XX	US2004034888-A1.	
XX	19-FEB-2004.	
XX	28-APR-2003; 2003US-00425114.	
XX	06-MAY-1999; 99US-00304517.	
PR	05-NOV-2001; 2001US-00985678.	
XX	(LIUJ/) LIU J.	
PA	(ZHOU/) ZHOU Y.	
PA	(KOVA/) KOVALIC D K.	
PA	(SCRE/) SCREEN S E.	
PA	(TABAS/) TABASKA J E.	
PA	(CAOY/) CAO Y.	
XX	Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;	
PI	WPI; 2004-180133/17.	
DR		
XX	New recombinant DNA construct, useful for improving plant tolerance to	
PT	cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or	
PT	pests, for conferring increased resistance to plant disease, or for	
PT	improving yield.	
XX		
PS	Claim 1; SEQ ID NO 32541; 15pp; English.	
XX		
CC	The invention describes a recombinant DNA construct comprising a	
CC	polynucleotide consisting of a sequence encoding an amino acid sequence	
CC	available in electronic form from the US patent office at	
CC	ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide	
CC	of the invention are also useful in physical arrays of molecules and as	
CC	plant breeding markers. The recombinant DNA construct is useful for	
CC	improving plant tolerance to cold, heat, drought, herbicides, extreme	
CC	osmotic conditions, pathogens or pests, for manipulating growth rate in	
CC	plant cells by modification of the cell cycle pathway, for conferring	
CC	increased resistance to plant disease, for producing galactomannan,	
CC	lignin or plant growth regulators, for increasing the rate of homologous	
CC	recombination in plants, for improving yield by modification of	
CC	photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake	
CC	or by providing improved plant growth and development under at least one	
CC	stress condition or for modifying seed oil or protein yield and/or	
CC	content. This sequence represents a plant full length insert	
CC	polynucleotide that can be used in the recombinant DNA construct of the	
XX	invention.	

GenCore version 5.1.7

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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 09:51:22 ; Search time 4261 Seconds
(without alignments)

10979.151 Million cell updates/sec

Title: US-10-660-208-90

Perfect score: 823

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba.*

2: gb_in.*

3: gb_env.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pr.*

9: gb_ro.*

10: gb_sts.*

11: gb_sy.*

12: gb_un.*

13: gb_vi.*

14: gb_htg.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	823	100.0	823	6	AX299949 Sequence
2	564	68.5	1587	6	AX299946 Sequence
3	252	30.6	149882	14	AC155395 Sequence
4	251.8	30.6	182004	14	AC155608 Zea mays
5	249.8	30.4	110000	15	Continuation (2 of
6	242.6	29.5	193326	14	AC155578 Zea mays
7	241.2	29.3	148120	14	AC155517 Zea mays
8	236	28.7	112468	14	AC149836 Zea mays
9	236	28.7	143793	14	AC149827 Zea mays
10	235.2	28.6	1257	15	AF348367 Zea mays
11	234.4	28.5	117844	14	AC155360 Zea mays
12	234.4	28.5	170318	14	AC155367 Zea mays
13	227	27.6	6343	15	ZMGLOSSY
14	226.4	27.5	134692	14	AC151050 Zea mays
15	223.2	27.1	198102	14	AC145389 Zea mays
16	220	26.7	133685	14	AC155399 Zea mays
17	218.4	26.5	175006	14	AC155579 Zea mays
18	215.2	26.1	164241	14	AC155575 Zea mays

c	19	213.6	26.0	189962	14	AC148165
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	21	209.2	25.4	6550	6	BD132692
	22	209.2	25.4	6550	6	AR208995
	23	209.2	25.4	6550	6	AR482064
	24	209.2	25.4	9299	6	BD132705
	25	209.2	25.4	9299	6	AR209008
	26	209.2	25.4	9299	6	AR482077
	27	209.2	25.4	9408	6	BD132706
	28	209.2	25.4	9408	6	AR209009
	29	209.2	25.4	9408	6	AR482078
	30	208.4	25.3	116794	14	AC149633
	31	205.8	25.0	187674	14	AC149640
c	32	202.4	24.6	169976	15	AY883559
	33	194	23.6	181757	14	AC146713
	34	193.4	23.5	160351	14	AC148152
	35	186	22.6	147470	15	AC157776
	36	173	21.0	119531	14	AC155407
c	37	164.6	20.0	69497	14	AC149816
c	38	143.6	17.4	165688	14	AC155607
c	39	141.6	17.2	132900	14	AC166637
	40	110.2	13.4	720	6	AR649754
	41	110.2	13.4	720	6	AX406847
c	42	84.2	10.2	166981	14	AC145225
	43	83.2	10.1	174838	14	AC155493
c	44	67.4	8.2	181475	14	AC155391
c	45	62	7.5	154044	14	AC150186

ALIGNMENTS

RESULT 1
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LOCUS Sequence 90 from Patent WO0183790.
DEFINITION AX299949
ACCESSION AX299949
VERSION AX299949.1 GI:17129440
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE
1
AUTHORS Conner, T.W., Dubois, P., Malven, M. and Masucci, J.D.
TITLE Plant regulatory sequences for selective control of gene expression
JOURNAL Patent: WO 0183790-A 90 08-NOV-2001;
Monsanto Technology LLC (US)
FEATURES
Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 823; DB 6; Length 823;
Best Local Similarity 100.0%; Pred. No. 6.6e-219; Indels 0; Gaps 0;
Matches 823; Conservative 0; Mismatches 0;
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1 CTGCAGGTACTCCAAGTATAGACACAGCTAAACACACATAATGCGAGTGTGTCATGTC 60
DB 1 TAAACATGTCCTTACCATTATGTTATCAATCAGAACATTCAATAAATAAGTGA 120
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QY 121 CCAATCAGATAGTCTCTGTCGCGATATAGACACTGCTGCTTCGTCAGATGA 180
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QY 181 CATGCTTCGAGATTTTTCATTACATTCACCCCTTAGACACACTCTTAAGACACAACTTAAGAC 240

Center name: TIGR	
Seq_lib_id: ZGGR	
----- Project information	
Web site: http://www.tigr.org/tdb/tgi/maize/	
Contact: maize@tigr.org	

* NOTE: This is a 'working draft' sequence. It currently	
* consists of 31 contigs. The true order of the pieces	
* is not known and their order in this sequence record is	
* arbitrary. Gaps between the contigs are represented as	
* runs of N, but the exact sizes of the gaps are unknown.	
* This record will be updated with the finished sequence	
* as soon as it is available and the accession number will	
* be preserved.	

1	2004: contig of 2004 bp in length
2005	2104: gap of unknown length
2105	15140: contig of 13036 bp in length
15141	15240: gap of unknown length
15241	16541: contig of 1301 bp in length
16542	16641: gap of unknown length
16642	21576: contig of 4935 bp in length
21577	21676: gap of unknown length
21677	24623: contig of 2947 bp in length
24624	24723: gap of unknown length
24724	28116: contig of 3393 bp in length
28117	28216: gap of unknown length
28217	29534: contig of 1318 bp in length
29535	29634: gap of unknown length
29635	32648: contig of 3014 bp in length
32649	32748: gap of unknown length
32749	40512: contig of 7764 bp in length
40513	40612: gap of unknown length
40613	43861: contig of 3249 bp in length
43862	43961: gap of unknown length
43962	48429: contig of 4468 bp in length
48430	48529: gap of unknown length
48530	59229: contig of 10700 bp in length
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59330	60889: contig of 1560 bp in length
60890	60989: gap of unknown length
60990	65147: contig of 4158 bp in length
65148	65247: gap of unknown length
65248	67580: contig of 2333 bp in length
67581	67680: gap of unknown length
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123010	127130: contig of 4121 bp in length
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140194	162843: contig of 22650 bp in length
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162944	167186: contig of 4243 bp in length
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169331	170030: gap of unknown length
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175432	175531: gap of unknown length
175532	177305: contig of 1774 bp in length
177306	177405: gap of unknown length
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gap	178664 178763: gap of unknown length
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Best Local Similarity	93.9%; Pred. No. 4.8e-59;

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Db 47334 TAAACATGTGCTTATCATATTCATTTATCAATCAAGACAACTTCAATAAATTAAGTGA 47393
Qy 121 CCAATCAGATAGTCTCTGTCGCGAATATAGAGTAAAGACACTGTGTTCTTCGTCGAAGATA 180
Db 47394 CCAATCAGATAGTCTCTGTCGCGAATATAGAGTAAAGACACTGTGTTCTTCGTCGAAGATA 47453
Qy 181 CATGCTTGAGATTTTACATTCACCCCTAGACACACTCTTAAGACACAACTTAAGAC 240
Db 47454 CGTGTCTTGAGATTTTACATTCACCCCTAGACACACTCTTAAGACACAACTTAAGAC 47513
Qy 241 ACCATTGTACATGCGCTTAACTGGCAGCGCTACGTAGGG 279
Db 47514 ACCATTGTACATGCGCTTAACTGGCAGCGCTACGTAGGG 47552

RESULT 5
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WPCOMMENT
Sequence split into 4 fragments LOCUS AY664417 Accession AY664417
Fragment Name Begin End
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AY664417_1 100001 210000
AY664417_2 200001 310000
AY664417_3 300001 366120
Continuation (2 of 4) of AY664417 from base 100001 (AY664417 Zea mays cultivar Mol1 locu

Query Match 30.4%; Score 249.8; DB 15; Length 110000;
Best Local Similarity 93.9%; Pred. No. 1.7e-58;
Matches 260; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
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Qy 121 CCAATCAGATAGTCTCTGTCGCGAATATAGAGTAAAGACACTGTGTTCTTCGTCGAAGATA 180
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Qy 181 CATGCTTGAGATTTTACATTCACCCCTAGACACACTCTTAAGACACAACTTAAGAC 240
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Qy 241 ACCATTGTACATGCGCTTAACTGGCAGCGCTACGTAG 277
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RESULT 6
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DEFINITION Zea mays strain B73 clone ZMBB0190D10, *** SEQUENCING IN PROGRESS
***, 34 unordered pieces.
ACCESSION AC155578
VERSION AC155578.2 GI:58082437
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 193326)
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Chan, A.P., Perle, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlffing, T.,
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J., and
Quackenbush, J.
Consortium for Maize Genomics - BAC skin sequencing and assembly
Unpublished
2 (bases 1 to 193326)
Chan, A.P., Perle, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlffing, T.,
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J., and
Quackenbush, J.
Direct Submission
Submitted (15-JAN-2005) The Institute for Genomic Research (TIGR),
9712 Medical Center Dr, Rockville, MD 20850
3 (bases 1 to 193326)
Chan, A.P., Perle, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlffing, T.,
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J., and
Quackenbush, J.
Direct Submission
Submitted (25-JAN-2005) The Institute for Genomic Research (TIGR),
9712 Medical Center Dr, Rockville, MD 20850
On Jan 25, 2005 this sequence version replaced gi:57863099.
----- Trace submission
Center name: TIGR
Seq lib id: ZGES
----- Project information
Web site: http://www.tigr.org/tdb/cgi/maize/
Contact: maize@tigr.org
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 34 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 2168: contig of 2168 bp in length
* 2 2169: gap of unknown length
* 3 2269: contig of 5678 bp in length
* 4 7947: gap of unknown length
* 5 8047: gap of 6485 bp in length
* 6 14531: contig of 6485 bp in length
* 7 14532: gap of unknown length
* 8 23005: contig of 8374 bp in length
* 9 23006: gap of unknown length
* 10 23105: gap of unknown length
* 11 23106: contig of 8086 bp in length
* 12 31191: gap of unknown length
* 13 31192: gap of unknown length
* 14 31292: contig of 9184 bp in length
* 15 40575: gap of unknown length
* 16 40576: contig of 4765 bp in length
* 17 45340: gap of unknown length
* 18 45341: gap of 4799 bp in length
* 19 45441: contig of 4799 bp in length
* 20 50240: gap of unknown length
* 21 50340: contig of 5369 bp in length
* 22 55709: gap of unknown length
* 23 55809: contig of 10782 bp in length
* 24 66591: gap of unknown length
* 25 66591: contig of 7785 bp in length
* 26 74475: gap of unknown length
* 27 74476: contig of 9714 bp in length
* 28 84290: gap of unknown length
* 29 84390: contig of 2297 bp in length
* 30 86686: gap of unknown length
* 31 86687: contig of 2607 bp in length
* 32 86787: gap of unknown length
* 33 89394: gap of unknown length
* 34 89494: contig of 9902 bp in length
* 35 99396: gap of unknown length
* 36 99496: contig of 5295 bp in length
* 37 104790: contig of 5295 bp in length
* 38 104791: gap of unknown length
```


Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
AUTHORS

Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
Quackenbush, J.

Consortium for Maize Genomics - BAC skim sequencing and assembly

TITLE
JOURNAL
REFERENCE
AUTHORS

Unpublished
2 (bases 1 to 148120)
Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
Quackenbush, J.

Direct Submission

TITLE
JOURNAL

Submitted (15-JAN-2005) The Institute for Genomic Research (TIGR),
9712 Medical Center Dr, Rockville, MD 20850

REFERENCE
AUTHORS

3 (bases 1 to 148120)
Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
Quackenbush, J.

Direct Submission

TITLE
JOURNAL

Submitted (25-JAN-2005) The Institute for Genomic Research (TIGR),
9712 Medical Center Dr, Rockville, MD 20850

COMMENT

On Jan 25, 2005 this sequence version replaced gi:57863038.

----- Trace submission

Center name: TIGR

Seq lib id: ZOBH

----- Project information

Web site: <http://www.tigr.org/tdb/tgi/maize/>

Contact: maize@tigr.org

* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 7711: contig of 7711 bp in length
* 7712 7811: gap of unknown length
* 7812 38165: contig of 30354 bp in length
* 38166 38265: gap of unknown length
* 38266 40248: contig of 1983 bp in length
* 40249 40348: gap of unknown length
* 40349 55752: contig of 15404 bp in length
* 55753 55852: gap of unknown length
* 55853 61693: contig of 5841 bp in length
* 61694 79902: contig of 18109 bp in length
* 79903 80002: gap of unknown length
* 80003 82646: contig of 2644 bp in length
* 82647 82746: gap of unknown length
* 82747 98869: contig of 16123 bp in length
* 98870 98969: gap of unknown length
* 98970 102329: contig of 3360 bp in length
* 102330 102429: gap of unknown length
* 102430 105931: contig of 3502 bp in length
* 105932 106031: gap of unknown length
* 106032 124298: contig of 18267 bp in length
* 124299 124398: gap of unknown length
* 124399 125579: contig of 1181 bp in length
* 125580 125679: gap of unknown length
* 125680 130751: contig of 5072 bp in length
* 130752 130852: gap of unknown length
* 130853 144420: contig of 13569 bp in length
* 144421 144520: gap of unknown length
* 144521 148120: contig of 3600 bp in length.

FEATURES
source

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/strain="B73"
/db_xref="taxon:4577"
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38166..38265
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55753..55852
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105932..106031
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124299..124398
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125580..125679
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130752..130851
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144421..144520
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ORIGIN

Query Match 29.38; Score 241.2; DB 14; Length 148120;
Best Local Similarity 95.0%; Pred.No.4.e-56;
Matches 249; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
Qy 1 CTGCACGGTACTCAAGTATAAGACACAGCTAAACACACATTAATCAAGTGC 60
Db 145976 CTGCACGGTACTCAAGTATAAGACACAGCTAAACACACATTAATCAAGTGC 145917
Qy 61 TAAACATGCTCTTACCATTATTCATTAATCAAGACATTAATTAAGTGA 120
Db 145916 TAAACATGCTCTTACCATTATTCATTAATCAAGACATTAATTAAGTGA 145857
Qy 121 CCAATCAGATAGTCTCTGTCCTCCGATATAGAGCTAGACACTGTGCTTCGTCGAAGATA 180
Db 145856 CCAATCAGTACGCTCTCTGTCCTCGAATAGAGCTAGACACTGTGCTTCGTCGAAGATA 145797
Qy 181 CATGCTCTGAGATTTTTCATATTCACCCCTAGACACACTCTTAAGACACAACTTAAGAC 240
Db 145796 CATGCTCTGAGTTTTCATATTCACCCCTAGACACACTCTTAAGACACAACTTAAGAC 145737
Qy 241 ACCATGTACATGCCCTAACT 262
Db 145736 ACTCATTTGATACGCCCTTAGT 145715

RESULT 8

AC149836

LOCUS

DEFINITION

AC149836

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AC149836

Zea mays clone ZMMBc0496L17, *** SEQUENCING IN PROGRESS ***; 2

ordered pieces.

AC149836

AC149836.2 GI:57790161

HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.

Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

AC149836 112468 bp DNA linear HTG 03-FEB-2005

Zea mays clone ZMMBc0496L17, *** SEQUENCING IN PROGRESS ***; 2

ordered pieces.

AC149836

AC149836.2 GI:57790161

HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.

Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Menus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (22-JUN-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 143793)

TITLE JOURNAL REFERENCE AUTHORS

FEATURES
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/organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"
/clone="ZMMB0051H21"
/clone_lib="CHORI-201 Maize B73 BAC EcoRI Library"
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/estimated_length=unknown
36274..36373
/estimated_length=unknown
45583..45682
/estimated_length=unknown
78485..78584
/estimated_length=unknown
99757..99856
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120941..121040
/estimated_length=unknown
123151..123250
/estimated_length=unknown

ORIGIN

Query Match 28.78; Score 236; DB 14; Length 143793;
Best Local Similarity 94.28; Pred No. 1.3e-54;
Matches 245; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 CTGCACGGTACTCCCAAGTATAAGACACAGCTAAACACACATTAATGCAGTGGTCAATGTC 60
Db 29159 CTGCACGGTACTCCCAAGTATAAGACACAGCTAAACACACATTAATGCAGTGGTCAATGTC 29100
Qy 61 TAAACATGTCCTTACCATATTCATTTGATCAATCAATCAAGACATTAATTAAGTGA 120
Db 29099 TAAACATGTCCTTACCATATTCATTTGATCAATCAATCAAGACATTAATTAAGTGA 29040
Qy 121 CCAATCAGATAGTCTCTGTCCTCCGAATATAGAGCTTAAGACACTGTCTCTCGTCAAGATA 180
Db 29039 CCAATCAGTACCTCTTGTCTCGAATATAGAGCTTAAGACACTGTCTCTCGTCAAGATA 28980
Qy 181 CATGCTTTGAGATTTTTTACATTCACCCCTTAGACACACTCTTAAGACACAACACTTAAGAC 240
Db 28979 CATGCTTTGAGATTTTTTACATTCACCCCTTAGACACACTCTTAAGACACAACACTTAAGAC 28920
Qy 241 ACCATTGTACATGCCCTAA 260
Db 28919 ACTCATTTGATCGCCCTTA 28900

RESULT 10
AF348367/c
LOCUS
DEFINITION Zea mays inbred B77 beta-keto acyl reductase gene, partial cds.
ACCESSION AF348367
VERSION AF348367.1 GI:19070512

TITLE JOURNAL COMMENT

Submitted (03-FEB-2005) Broad Institute of MIT and Harvard, 320 Charles Street, Cambridge, MA 02141, USA
On Jan 14, 2005 this sequence version replaced gi:49035053.
All repeats were identified using RepeatMasker.
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center
Center: Broad Institute of MIT and Harvard
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@broad.mit.edu

Bharti, AK and Messing, J: The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers, The State University of New Jersey, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA (http://pgir.rutgers.edu)
Butler, E and Wang, R: Arizona Genomics Institute, Biological Sciences West, 448A, P.O. Box 210088, University of Arizona, Tucson, AZ 85721, USA (http://www.genome.arizona.edu)

Project Information
Center project name: L30279
Center clone name: 51_H_21

* NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
* 1 30907: contig of 30907 bp in length
* 30908 31007: gap of unknown length
* 31008 36273: contig of 5266 bp in length
* 36274 36373: gap of unknown length
* 36374 45582: contig of 9209 bp in length
* 45583 45682: gap of unknown length
* 45683 78484: contig of 32802 bp in length
* 78485 78584: gap of unknown length
* 78585 99756: contig of 21172 bp in length
* 99757 99856: gap of unknown length
* 99857 120940: contig of 21084 bp in length
* 120941 121040: gap of unknown length
* 121041 123150: contig of 2110 bp in length
* 123151 123250: gap of unknown length
* 123251 143793: contig of 20543 bp in length.
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/mol_type="genomic DNA"
/db_xref="taxon:4577"
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/clone_lib="CHORI-201 Maize B73 BAC EcoRI Library"
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36274..36373
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45583..45682
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78485..78584
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99757..99856
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123151..123250
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[illegible]


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* 28151 30686: contig of 2536 bp in length
* 30687 gap of unknown length
* 32491: contig of 1705 bp in length
* 32492 gap of unknown length
* 32591: gap of unknown length
* 42096: contig of 9505 bp in length
* 42097 gap of unknown length
* 42196: gap of unknown length
* 80810: contig of 38614 bp in length
* 80811 gap of unknown length
* 100759: contig of 19849 bp in length
* 100760 gap of unknown length
* 100859: gap of unknown length
* 102668: contig of 1809 bp in length
* 102669 gap of unknown length
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* 110690: contig of 7922 bp in length
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* 110790: gap of unknown length
* 114348: contig of 3558 bp in length
* 114349 gap of unknown length
* 114449: gap of unknown length
* 117461: contig of 3013 bp in length
* 117462 gap of unknown length
* 117561: gap of unknown length
* 117562 gap of unknown length
* 117569: contig of 2138 bp in length
* 117570 gap of unknown length
* 117999: gap of unknown length
* 122051: contig of 2252 bp in length
* 122052 gap of unknown length
* 122151: gap of unknown length
* 124115: contig of 2164 bp in length
* 124116 gap of unknown length
* 124117: gap of unknown length
* 124118: contig of 3496 bp in length
* 124119 gap of unknown length
* 128011: gap of unknown length
* 128012 gap of unknown length
* 129528: contig of 1517 bp in length
* 129529 gap of unknown length
* 129628: gap of unknown length
* 132542: contig of 2914 bp in length
* 132543 gap of unknown length
* 132642: gap of unknown length
* 134392: contig of 1750 bp in length
* 134393 gap of unknown length
* 134796: gap of unknown length
* 137476: contig of 2984 bp in length
* 137477 gap of unknown length
* 137576: gap of unknown length
* 138544: contig of 968 bp in length
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* 146242: contig of 7598 bp in length
* 146243 gap of unknown length
* 146342: gap of unknown length
* 150461: contig of 4119 bp in length
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* 150561: gap of unknown length
* 158564: contig of 8103 bp in length
* 158565 gap of unknown length
* 158764: gap of unknown length
* 158765 170318: contig of 11554 bp in length.
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/strain="B73"
/db_xref="taxon:4577"
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8024..8123
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11192..11291
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14580..14679
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17731..17830
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20205..20304
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26300..26399
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32492..32591
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FEATURES

source

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Best Local Similarity 93.8%; Pred. No. 3.5e-54;
Matches 244; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 CTGCACGGTACTCCAAAGTATTAAGACAGACAGCTTAAACCAACATATGCAGTGGTCATGTC 60
DB 99136 CTGCACAGTACTCCAAAGTATTAAGATACAACTTAAACCAACATATGCAGTGGTCATGTC 99195
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DB 99256 CCAATCAGTACTGCTCTCTGTCCTCGAATATAGAGCTAGAGACTGTGTTGTCAGAGATA 99315
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DB 99316 CGTGTCTTGAGTTTTTTTACATTCACCCCTAGACACACTCTTAAGACACAACTTAAAGAC 99375
QY 241 ACCCATGTACATGCCCTAA 260
DB 99376 ACCCATGTACATGCCCTAA 99395

RESULT 13
LOCUS ZMGLOSSY
DEFINITION Z.mays Glossy2 locus DNA.
ACCESSION X88779
VERSION X88779.1 GI:949979
KEYWORDS
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SOURCE
ORGANISM
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1

REFERENCE
AUTHORS
Tacke, E., Korfhage, C., Michel, D., Maddaloni, M., Motto, M.,
Lanzini, S., Salamini, F. and Doring, H.P.
Transposon tagging of the maize Glossy2 locus with the transposable
element En/Spm
Plant J. 8 (6), 907-917 (1995)

TITLE
JOURNAL
PUBMED
8580961
2 (bases 1 to 6343)
Direct Submission
Tacke, E.
Submitted (19-JUN-1995) E. Tacke, Max-Planck-Institute, Dept.
Salamini, Carl-von-Linne-Weg 10, 50829 Koeln, NRW, FRG

FEATURES
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/number=1
3924..5001
/number=2

intron
exon

ORIGIN
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Matches 247; Conservative 0; Mismatches 15; Indels 1; Gaps 1;
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Qy 61 TAAACATGTGTTTACCATATTCATTCATCAATCAATCAAGAACATTCATTAAGTGA 120
Db 3675 TAAACATGTGTTTACCATATTCATTCATCAATCAATCAAGAACATTCATTAAGTGA 3734
Qy 121 CCAATCAGATAGTCTCTGTCCTCCGATATAGCTTAGACACTGTGTTCTGTCAGATA 180
Db 3735 CCAATCAGATAGTCTCTGTCCTCCGATATAGCTTAGACACTGTGTTCTGTCAGATA 3794
Qy 181 CATGCTTGAGATTTTACATTCACCCCTAGACACACTCTTAAGACACAACTTAAGAC 240
Db 3795 CATGCTTGAGATTTTACATTCACCCCTAGACACACTCTTAAGACACAACTTAAGAC 3854
Qy 241 A-CCATTGTATGCCCTCAACT 262
Db 3855 ACCCCACGGTACATGCCCTCAACT 3877

RESULT 14
AC151050
LOCUS
DEFINITION
AC151050
AC151050.2 GI:57790152
HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 134692)
Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K.
and Messing, J.
Zea mays, clone ZMMB0243P06
Unpublished
2 (bases 1 to 134692)
Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K.,
Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S.,
Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L.,
Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., Corum, B., DeAtellano, K., Diaz, J.S., Dodge, S.,
Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P.,
Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L.,
Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J.,
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P.,
Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C.,
Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
Talamas, J., Tefaye, S., Theodore, J., Topham, K., Travers, M.,
Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (19-AUG-2004) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 134692)
Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K.,
Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S.,
Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L.,
Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., Corum, B., DeAtellano, K., Diaz, J.S., Dodge, S.,
Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P.,
Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L.,
Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J.,
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P.,
Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
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Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C.,
Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
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Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
Submitted (03-FEB-2005) Broad Institute of MIT and Harvard, 320
Charles Street, Cambridge, MA 02141, USA
On Jan 14, 2005 this sequence version replaced gi:51372063.
All repeats were identified using RepeatMasker:
Smit, A.P.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center
Center: Broad Institute of MIT and Harvard
Center code: WIGR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@broad.mit.edu

Bharti, AK and Messing, J: The Plant Genome Initiative at
Rutgers, Wakeman Institute, Rutgers, The State University of New
Jersey, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA
(http://pgr.rutgers.edu)
Butler, E and Wing, R: Arizona Genomics Institute, Biological
Sciences West, 448A, P.O. Box 210088, University of Arizona,
Tucson, AZ 85721, USA (http://www.genome.arizona.edu)

----- Project Information

Center project name: L30292
Center clone name: 243_P_6

* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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* 21092 21191: gap of unknown length
* 21192 26635: contig of 5444 bp in length
* 26636 26735: gap of unknown length
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* 65464 65563: gap of unknown length
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* 69590 69689: gap of unknown length
* 69690 75792: contig of 6103 bp in length
* 75793 75892: gap of unknown length
* 75893 78948: contig of 3056 bp in length
* 78949 81704: gap of unknown length
* 81705 81804: gap of unknown length
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* 89600 89699: gap of unknown length
* 89700 95873: contig of 6174 bp in length
* 95874 95974: gap of unknown length
* 95974 121769: contig of 25796 bp in length
* 121770 121869: gap of unknown length
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* 131797 131896: gap of unknown length
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Matches 239; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

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Qy 182 ATGCTTTGAGATTTTTTACATTTACACCTTACACCTTACACACTTAAAGACACA 241
Db 57807 ATGCTTTGAGATTTTTTACATTTACCTCCGCTAGACACTCGAAGACACA 57866
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Db 57867 CCCATTGTACATGCCCTAAC 57886
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RESULT 15

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LOCUS Zea mays clone ZMMBBc0054A01, *** SEQUENCING IN PROGRESS ***, 4
DEFINITION ordered pieces.
ACCESSION AC145389
VERSION AC145389.6 GI:48762556
KEYWORDS HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 198102)
AUTHORS Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K.
and Messing, J.
TITLE Zea mays, clone ZMMBBc0054A01
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 198102)
AUTHORS Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
Boguslavsky, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,
Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K.,
Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
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Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hegos, B.,
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Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C.,
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Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
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Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (01-JUL-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 198102)

Barren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A. K., Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S., Arachchi, H. M., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArelano, K., Diaz, J. S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kanat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Menes, L., Mihova, T., Miha, V., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (20-JUN-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jun 16, 2004 this sequence version replaced gi:48717652.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center
Center: Whitehead Institute/MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@broad.mit.edu

Bharti, AK and Messing, J: The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers, The State University of New Jersey, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA
(<http://pgir.rutgers.edu>)
Butler, E and Wing, R: Arizona Genomics Institute, Biological Sciences West, 448A, P.O. Box 210088, University of Arizona, Tucson, AZ 85721, USA (<http://www.genome.arizona.edu>)
----- Project Information
Center project name: L29613
Center clone name: 54.A.1
----- Consensus Information
This consensus is derived from a shotgun assembly that has been manually curated. It is the best representation of the BAC that we can generate without further laboratory work. The draft assembly has been edited, and if possible, ends identified by vector as well as by BAC end sequences, and contigs ordered and oriented. Bases that are not Ns are either above Q20 or manually edited. This assembly was performed with phrap. All trace files for this project are available at the NCBI trace repository (<http://www.ncbi.nlm.nih.gov/Traces/trace.fcgi?>). An exact list of reads used in this assembly are available at <http://www.broad.mit.edu/annotation/plants/maize/randomclones.html>.

----- NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.

* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 1 20266: contig of 20266 bp in length
* 20267 20366: gap of 100 bp
* 20367 78634: contig of 58268 bp in length
* 78635 78734: gap of 100 bp
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/db_xref="taxon:4577"
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Best Local Similarity 91.2%; Pred. No. 4.0e-51;
Matches 248; Conservative 0; Mismatches 23; Indels 1; Gaps 1;
QY 2 TGACCGGTACTCCAAAGTATAGACACACAGCTAAACACACATATGCAAGTGTCTGCT 61
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DB 173718 CCCACTGTACATGCCCTTAGAGCTGCCGCTGC 173749


Search completed: March 5, 2006, 11:12:25
Job time : 4265 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocellera Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 11:24:36 ; Search time 862 Seconds
(without alignments)
7895.241 Million cell updates/sec

Title: US-10-660-208-90
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Scoring table: 
Gapop 60.0, Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA Main.*

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- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	75	9.1	1251	8	US-10-425-115-13680
7	73	8.9	859	8	US-10-425-115-13670
8	70	8.5	836	8	US-10-425-115-13673
9	66	8.0	894	8	US-10-425-115-13677
10	63	7.7	485	7	US-10-425-114-23949
11	63	7.7	814	8	US-10-425-115-134827
12	62	7.5	821	7	US-10-425-114-16472
13	59	7.2	791	7	US-10-425-114-12914
14	59	7.2	795	7	US-10-425-114-12891
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16	49	6.0	781	7	US-10-425-114-16676
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ALIGNMENTS

RESULT 1
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; Sequence 90, Application US/09846903
; Publication No. US20030200565A1
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Dubois, Patrice
; APPLICANT: Malven, Marianne
; APPLICANT: Masucci, James D.
; TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL
; TITLE OF INVENTION: OF GENE EXPRESSION
; FILE REFERENCE: 38-21(15678)B Promoters
; CURRENT APPLICATION NUMBER: US/09/846,903
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/201,255
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 90
; LENGTH: 823
; TYPE: DNA
; ORGANISM: Zea mays
US-09-846-903-90

Query Match 100.0%; Score 823; DB 3; Length 823;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 823; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 361 TGCAGCTCAATTCATAGAGCAAAACAGTGTAGAACCGCTATAAGCAATTAAGCAACA 420
 421 AGCGAACTATTGCTTAGCTACAACTTATAGCGAGGCGCCCAAGGCCCATCTTCGAGGT 480
 421 AGCGAACTATTGCTTAGCTACAACTTATAGCGAGGCGCCCAAGGCCCATCTTCGAGGT 480
 481 GTGGCTGCATATGCTGAAATTAAGCGAGGCGCCCAAGGCCCATCTTCGAGGT 540
 481 GTGGCTGCATATGCTGAAATTAAGCGAGGCGCCCAAGGCCCATCTTCGAGGT 540
 541 CAGCAATTGCTTTTGTAACTGCTCGATTAATTTGTTCACTTAAATAGACCACTTCAA 600
 541 CAGCAATTGCTTTTGTAACTGCTCGATTAATTTGTTCACTTAAATAGACCACTTCAA 600
 601 TTCTGTTCTAGTCAACATGCTCGATCCAGCGGGGAGGAGGAGCAATGTTGGGCC 660
 601 TTCTGTTCTAGTCAACATGCTCGATCCAGCGGGGAGGAGGAGCAATGTTGGGCC 660
 661 GCCGAGTGAGGCCAAGCGGCGGCTCGATCCAGCGGGGAGGAGGAGCAATGTTGGGCC 720
 661 GCCGAGTGAGGCCAAGCGGCGGCTCGATCCAGCGGGGAGGAGGAGCAATGTTGGGCC 720
 721 ATATACACAGCGCAGTACCATATCGTGTGTAGAGCAACTGAAACAGCCGAGC 780
 721 ATATACACAGCGCAGTACCATATCGTGTGTAGAGCAACTGAAACAGCCGAGC 780
 781 GATCTCTCTCCCTCTCCCTCTCCGATCCATCTCCAGCGCAG 823
 781 GATCTCTCTCCCTCTCCCTCTCCGATCCATCTCCAGCGCAG 823

RESULT 2
 US-10-660-208-90
 ; Sequence 90, Application US/10660208
 ; Publication No. US20040133946A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Conner, Timothy W.
 ; APPLICANT: Dubois, Patrice
 ; APPLICANT: Malven, Marianne
 ; APPLICANT: Masucci, James D.
 ; TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL
 ; FILE REFERENCE: 38-21(15678)B promoters
 ; CURRENT APPLICATION NUMBER: US/10/660,208
 ; CURRENT FILING DATE: 2003-09-11
 ; PRIOR APPLICATION NUMBER: US 60/201,255
 ; PRIOR FILING DATE: 2000-05-01
 ; NUMBER OF SEQ ID NOS: 98
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 90
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 US-10-660-208-90
 Query Match 100.0%; Score 823; DB 7; Length 823;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 823; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 CTGACGGTACTCCAAAGTATAGACACAGCTAAACACACATATGCGTGTATGTC 60
 1 CTGACGGTACTCCAAAGTATAGACACAGCTAAACACACATATGCGTGTATGTC 60
 61 TAAACATGCTTACCATATTCTTGTATCAATCAGAACATTCATATAAATAAGTGA 120

61 TAAACATGCTTACCATATTCTTGTATCAATCAGAACATTCATATAAATAAGTGA 120
 121 CCAATCAGATAGTCTCTCTGTCGCCGAATATAGAGCTAGACACTGTGCTTCGTCAGATA 180
 121 CCAATCAGATAGTCTCTCTGTCGCCGAATATAGAGCTAGACACTGTGCTTCGTCAGATA 180
 181 CATGCTCTGAGATTTTTCATCATTACCCCTCTAGACACACTCTTAAGACACAACCTTAAGAC 240
 181 CATGCTCTGAGATTTTTCATCATTACCCCTCTAGACACACTCTTAAGACACAACCTTAAGAC 240
 241 ACCAATTGTATCAGTCCCTTAACCTGCGACCGCTACGTAGGGGCTATTCAAGAACCAACCATG 300
 241 ACCAATTGTATCAGTCCCTTAACCTGCGACCGCTACGTAGGGGCTATTCAAGAACCAACCATG 300
 301 TACAGTTGTGTCACGCTGAATGTTATTGCTTCAGATTAAGCTAAATATTAGACTGA 360
 301 TACAGTTGTGTCACGCTGAATGTTATTGCTTCAGATTAAGCTAAATATTAGACTGA 360
 361 TGCAGCTGCAATTCATAGAGCAAAACAGTGTAGAACCGCTATAAGCAATTAAGCAACA 420
 361 TGCAGCTGCAATTCATAGAGCAAAACAGTGTAGAACCGCTATAAGCAATTAAGCAACA 420
 421 AGCGAACTATTGCTTAGCTACAACTTATAGCGAGGCGCCCAAGGCCCATCTTCGAGGT 480
 421 AGCGAACTATTGCTTAGCTACAACTTATAGCGAGGCGCCCAAGGCCCATCTTCGAGGT 480
 481 GTGGCTGCATATGCTGAAATTAAGCGAGGCGCCCAAGGCCCATCTTCGAGGT 540
 481 GTGGCTGCATATGCTGAAATTAAGCGAGGCGCCCAAGGCCCATCTTCGAGGT 540
 541 CAGCAATTGCTTTTGTAACTGCTCGATTAATTTGTTCACTTAAATAGACCACTTCAA 600
 541 CAGCAATTGCTTTTGTAACTGCTCGATTAATTTGTTCACTTAAATAGACCACTTCAA 600
 601 TTCTGTTCTAGTCAACATGCTCGATCCAGCGGGGAGGAGGAGCAATGTTGGGCC 660
 601 TTCTGTTCTAGTCAACATGCTCGATCCAGCGGGGAGGAGGAGCAATGTTGGGCC 660
 661 GCCGAGTGAGGCCAAGCGGCGGCTCGTCCGTCACACCCCTCTCGTTTACTAT 720
 661 GCCGAGTGAGGCCAAGCGGCGGCTCGTCCGTCACACCCCTCTCGTTTACTAT 720
 721 ATATACACAGCGCAGTACCATATCGTGTGTAGAGCAACTGAAACAGCCGAGC 780
 721 ATATACACAGCGCAGTACCATATCGTGTGTAGAGCAACTGAAACAGCCGAGC 780
 781 GATCTCTCTCCCTCTCCCTCTCCGATCCATCTCCAGCGCAG 823
 781 GATCTCTCTCCCTCTCCCTCTCCGATCCATCTCCAGCGCAG 823

RESULT 3
 US-09-846-903-87
 ; Sequence 87, Application US/09846903
 ; Publication No. US20030200565A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Conner, Timothy W.
 ; APPLICANT: Dubois, Patrice
 ; APPLICANT: Malven, Marianne
 ; APPLICANT: Masucci, James D.
 ; TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL
 ; FILE REFERENCE: 38-21(15678)B promoters
 ; CURRENT APPLICATION NUMBER: US/09/846,903
 ; CURRENT FILING DATE: 2001-04-26
 ; PRIOR APPLICATION NUMBER: US 60/201,255
 ; PRIOR FILING DATE: 2000-05-01
 ; NUMBER OF SEQ ID NOS: 98
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 87
 ; LENGTH: 1587
 ; TYPE: DNA
 ; ORGANISM: Zea mays


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; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 13680
; LENGTH: 1251
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_112467C.1
US-10-425-115-13680

Query Match          9.1%; Score 75; DB 8; Length 1251;
Best Local Similarity 100.0%; Pred. No. 2.6e-30;
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 749 GTGGTGCTAGAGCAACTGAAACAGCGCGGATCTCTCTCCCTCTCCCTCTCCCGATC 808
Db 371 GTGGTGCTAGAGCAACTGAAACAGCGCGGATCTCTCTCCCTCTCCCTCTCCCGATC 430

Qy 809 CATTCTCCAGCGCAG 823
Db 431 CATTCTCCAGCGCAG 445

RESULT 7
US-10-425-115-13670
; Sequence 13670, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 13670
; LENGTH: 859
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_112458C.1
US-10-425-115-13670

Query Match          8.9%; Score 73; DB 8; Length 859;
Best Local Similarity 100.0%; Pred. No. 3.3e-29;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 751 GTGTCTAGAGCAACTGAAACAGCGCGGATCTCTCTCCCTCTCCCTCTCCCGATCCA 810
Db 10 GTGTCTAGAGCAACTGAAACAGCGCGGATCTCTCTCCCTCTCCCTCTCCCGATCCA 69

Qy 811 TTCTCCAGCGCAG 823
Db 70 TTCTCCAGCGCAG 82

RESULT 8
US-10-425-115-13673
; Sequence 13673, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants

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; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 13673
; LENGTH: 836
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_112460C.1
US-10-425-115-13673

Query Match          8.5%; Score 70; DB 8; Length 836;
Best Local Similarity 100.0%; Pred. No. 1.5e-27;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 754 GCTAGAGCAACTGAAACAGCGCGGATCTCTCTCCCTCTCCCTCTCCCGATCCA 813
Db 10 GCTAGAGCAACTGAAACAGCGCGGATCTCTCTCCCTCTCCCTCTCCCGATCCA 69

Qy 814 TCCAGCGCAG 823
Db 70 TCCAGCGCAG 79

RESULT 9
US-10-425-115-13677
; Sequence 13677, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 13677
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_112464C.1
US-10-425-115-13677

Query Match          8.0%; Score 66; DB 8; Length 894;
Best Local Similarity 100.0%; Pred. No. 2.5e-25;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 758 GAAGCAACTGAAACAGCGCGGATCTCTCTCCCTCTCCCTCTCCCGATCCA 817
Db 12 GAAGCAACTGAAACAGCGCGGATCTCTCTCCCTCTCCCTCTCCCGATCCA 71

Qy 818 GCGCAG 823
Db 72 GCGCAG 77

RESULT 10
US-10-425-114-23949/c
; Sequence 23949, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

```

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 23949

; LENGTH: 485

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3606-031-G10_FLI

US-10-425-114-23949

Query Match 7.7%; Score 63; DB 7; Length 485;

Best Local Similarity 100.0%; Pred. No. 1.1e-23;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 183 TGTCTTGAGATTTTACATTCACCCCTAGACACACTCTAAGACACAACTTAAGACAC 242

Db 362 TGTCTTGAGATTTTACATTCACCCCTAGACACACTCTAAGACACAACTTAAGACAC 303

Qy 243 CCA 245

Db 302 CCA 300

RESULT 11

US-10-425-115-134827/c

; Sequence 134827, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 134827

; LENGTH: 814

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: MET4577_54445C.1

US-10-425-115-134827

Query Match 7.7%; Score 63; DB 8; Length 814;

Best Local Similarity 100.0%; Pred. No. 1.2e-23;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 183 TGTCTTGAGATTTTACATTCACCCCTAGACACACTCTAAGACACAACTTAAGACAC 242

Db 690 TGTCTTGAGATTTTACATTCACCCCTAGACACACTCTAAGACACAACTTAAGACAC 631

Qy 243 CCA 245

Db 630 CCA 628

RESULT 12

US-10-425-114-16472

; Sequence 16472, Application US/10425114

; Publication No. US20040034888A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 16472

; LENGTH: 821

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3066-004-E5_FLI

US-10-425-114-16472

Query Match 7.5%; Score 62; DB 7; Length 821;

Best Local Similarity 100.0%; Pred. No. 4.2e-23;

Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 762 CAACCTGAAACAGCCGAGCGATCTCTCCCTCTCCGATCCATTCACGCGC 821

Db 1 CAACCTGAAACAGCCGAGCGATCTCTCCCTCTCCGATCCATTCACGCGC 60

Qy 822 AG 823

Db 61 AG 62

RESULT 13

US-10-425-114-12914

; Sequence 12914, Application US/10425114

; Publication No. US20040034888A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 12914

; LENGTH: 791

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: CC-ZMPO148069D04_FLI

US-10-425-114-12914

Query Match 7.2%; Score 59; DB 7; Length 791;

Best Local Similarity 100.0%; Pred. No. 1.9e-21;

Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 765 CTGAAACAGCCGAGCGATCTCTCCCTCTCCGATCCATTCACGCGC 823

Db 1 CTGAAACAGCCGAGCGATCTCTCCCTCTCCGATCCATTCACGCGC 59

RESULT 14

US-10-425-114-12891

; Sequence 12891, Application US/10425114

; Publication No. US20040034888A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

;; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

;; FILE REFERENCE: 38-21(53313)B

;; CURRENT APPLICATION NUMBER: US/10/425,114

;; CURRENT FILING DATE: 2003-04-28

;; NUMBER OF SEQ ID NOS: 73128

;; SEQ ID NO 12891

;; LENGTH: 795

;; TYPE: DNA

;; ORGANISM: Zea mays

;; FEATURE:

;; OTHER INFORMATION: Clone ID: CC-ZMPO148038E03_FLI

US-10-425-114-12891

Query Match 7.2%; Score 59; DB 7; Length 795;

Best Local Similarity 100.0%; Pred. No. 1.9e-21;

Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 765 CTGAAACAGCGGAGCGATCTCTCCCTCTCCGATCCATCTCCAGCGCAG 823

Db 1 CTGAAACAGCGGAGCGATCTCTCCCTCTCCGATCCATCTCCAGCGCAG 59

RESULT 15

US-10-425-115-39694

;; Sequence 39694, Application US/10425115

;; Publication No. US20040214272A1

;; GENERAL INFORMATION:

;; APPLICANT: La Rosa, Thomas J.

;; APPLICANT: Kovalic, David K.

;; APPLICANT: Zhou, Yihua

;; APPLICANT: Cao, Yongwei

;; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

;; FILE REFERENCE: 38-21(53222)B

;; CURRENT APPLICATION NUMBER: US/10/425,115

;; CURRENT FILING DATE: 2003-04-28

;; NUMBER OF SEQ ID NOS: 369326

;; SEQ ID NO 39694

;; LENGTH: 178

;; TYPE: DNA

;; ORGANISM: Zea mays

;; FEATURE:

;; NAME/KEY: unsure

;; LOCATION: (1)..(178)

;; OTHER INFORMATION: unsure at all n locations

;; FEATURE:

;; OTHER INFORMATION: Clone ID: MRT4577_136201C.1

US-10-425-115-39694

Query Match

Best Local Similarity 6.0%; Score 49; DB 8; Length 178;

Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 759 AAGCACTGAAACAGCGGAGCGATCTCTCCCTCTCCGATCCGAT 807

Db 18 AAGCACTGAAACAGCGGAGCGATCTCTCCCTCTCCGATCCGAT 66

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Job time : 862 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 11:26:37 ; Search time 509 Seconds
(without alignments)
3545.020 Million cell updates/sec

Title: US-10-660-208-90

Perfect score: 823

Sequence: 1 ctgacggtactccaagtat.....cgatccattctccagcgag 823

Scoring table: OligoNUC
Gapop 60.0, Gapext 60.0

Searched: 7218535 seqs, 1096242582 residues

Total number of hits satisfying chosen parameters: 14437070

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications NA New:

- 1: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq*
- 2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq*
- 3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq*
- 4: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq*
- 5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq*
- 6: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq*
- 7: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq*
- 8: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq*
- 9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq*
- 10: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq*
- 11: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq*
- 12: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq*
- 13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	22	2.7	1471	6	US-09-925-065A-35755
C 2	22	2.7	1617	6	US-09-925-065A-66476
C 3	22	2.7	1617	6	US-09-925-065A-66477
C 4	21	2.6	201	12	US-11-124-367A-26025
C 5	21	2.6	201	12	US-11-124-367A-26026
C 6	21	2.6	610	6	US-09-925-065A-546671
C 7	21	2.6	75782	7	US-10-330-773-772
C 8	21	2.6	390183	7	US-10-330-773-937
C 9	20	2.4	43103	8	US-10-995-561-13346
C 10	20	2.4	71207	7	US-10-330-773-416
C 11	20	2.4	100000	12	US-11-124-367A-5048
C 12	20	2.4	171936	8	US-10-933-025-24
C 13	20	2.4	194186	7	US-10-330-773-395
C 14	19	2.3	23	8	US-10-310-914A-1382480
C 15	19	2.3	201	8	US-10-995-561-17794
C 16	19	2.3	201	8	US-10-995-561-17868
C 17	19	2.3	201	8	US-10-995-561-18020
C 18	19	2.3	201	12	US-11-124-367A-17737
C 19	19	2.3	201	12	US-11-124-367A-17738
C 20	19	2.3	201	12	US-11-124-367A-24462

21	19	2.3	201	12	US-11-124-367A-24839	Sequence 24839, A
22	19	2.3	201	12	US-11-124-367A-25079	Sequence 25079, A
23	19	2.3	413	6	US-09-925-065A-4974	Sequence 4974, Ap
C 24	19	2.3	491	6	US-09-925-065A-917593	Sequence 917593, A
C 25	19	2.3	491	6	US-09-925-065A-917594	Sequence 917594, A
C 26	19	2.3	494	6	US-09-925-065A-141505	Sequence 141505, A
C 27	19	2.3	497	6	US-09-925-065A-327497	Sequence 327497, A
C 28	19	2.3	500	6	US-09-925-065A-930919	Sequence 930919, A
C 29	19	2.3	503	6	US-09-925-065A-746493	Sequence 746493, A
30	19	2.3	525	6	US-09-925-065A-796124	Sequence 796124, A
31	19	2.3	527	6	US-09-925-065A-254418	Sequence 254418, A
32	19	2.3	527	6	US-09-925-065A-254419	Sequence 254419, A
33	19	2.3	537	6	US-09-925-065A-787721	Sequence 787721, A
34	19	2.3	541	6	US-09-925-065A-168639	Sequence 168639, A
C 35	19	2.3	544	6	US-09-925-065A-570511	Sequence 570511, A
36	19	2.3	549	6	US-09-925-065A-20117	Sequence 20117, A
C 37	19	2.3	553	6	US-09-925-065A-141509	Sequence 141509, A
C 38	19	2.3	554	6	US-09-925-065A-21876	Sequence 21876, A
C 39	19	2.3	560	6	US-09-925-065A-939827	Sequence 939827, A
C 40	19	2.3	560	6	US-09-925-065A-939828	Sequence 939828, A
41	19	2.3	561	6	US-09-925-065A-413845	Sequence 413845, A
42	19	2.3	563	6	US-09-925-065A-793626	Sequence 793626, A
C 43	19	2.3	566	6	US-09-925-065A-653866	Sequence 653866, A
C 44	19	2.3	570	6	US-09-925-065A-732177	Sequence 732177, A
C 45	19	2.3	570	6	US-09-925-065A-811564	Sequence 811564, A

ALIGNMENTS

RESULT 1
US-09-925-065A-35755/c
; Sequence 35755, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35755
; LENGTH: 1471
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-35755

Query Match 2.7%; Score 22; DB 6; Length 1471;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 783 TCCTCTCCCTCCCTCCCTCC 804
|||||
Db 237 TCCTCTCCCTCCCTCCCTCC 216

RESULT 2
US-09-925-065A-66476/c
; Sequence 66476, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:

APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 66476
LENGTH: 1617
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-66476

Query Match 2.7%; Score 22; DB 6; Length 1617;
Best Local Similarity 100.0%; Pred. No. 0.16; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0;

QY 783 TCTCTCTCCCTCTCCCTCTCC 804
DB 331 TCTCTCTCCCTCTCCCTCTCC 310

RESULT 3

US-09-925-065A-66477/c
Sequence 66477, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:

APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
PRIOR FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 66477
LENGTH: 1617
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-66477

Query Match 2.7%; Score 22; DB 6; Length 1617;
Best Local Similarity 100.0%; Pred. No. 0.16; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 0;

QY 783 TCTCTCTCCCTCTCCCTCTCC 804
DB 331 TCTCTCTCCCTCTCCCTCTCC 310

RESULT 4

US-11-124-367A-26025/c

Sequence 26025, Application US/11124367A
Publication No. US20060024700A1
GENERAL INFORMATION:
APPLICANT: Michele Cargill
TITLE OF INVENTION: Genetic Polymorphisms Associated with
FILE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CL001519.ORD
CURRENT APPLICATION NUMBER: US/11/124,367A
PRIOR FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26025
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-11-124-367A-26025

Query Match 2.6%; Score 21; DB 12; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.48; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

QY 784 CTCCTCTCCCTCTCCCTCTCC 804
DB 24 CTCCTCTCCCTCTCCCTCTCC 4

RESULT 5

US-11-124-367A-26026/c
Sequence 26026, Application US/11124367A
Publication No. US20060024700A1
GENERAL INFORMATION:

APPLICANT: Michele Cargill
TITLE OF INVENTION: Genetic Polymorphisms Associated with
FILE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
FILE REFERENCE: CL001519.ORD
CURRENT APPLICATION NUMBER: US/11/124,367A
PRIOR FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,846
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/582,609
PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/599,554
PRIOR FILING DATE: 2004-08-09
NUMBER OF SEQ ID NOS: 34460
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26026
LENGTH: 201
TYPE: DNA
ORGANISM: Homo sapiens
US-11-124-367A-26026

Query Match 2.6%; Score 21; DB 12; Length 201;
Best Local Similarity 100.0%; Pred. No. 0.48; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 0;

QY 784 CTCCTCTCCCTCTCCCTCTCC 804
DB 169 CTCCTCTCCCTCTCCCTCTCC 149

RESULT 6

US-09-925-065A-546671/c
Sequence 546671, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:

APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 546671
LENGTH: 610
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-546671

Query Match 2.6%; Score 21; DB 6; Length 610;
Best Local Similarity 100.0%; Pred. No. 0.52;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 785 TCCTCTCCCTCTCCCTCTCCG 805
Db 548 TCCTCTCCCTCTCCCTCTCCG 528

RESULT 7
US-10-330-773-772/c
Sequence 772, Application US/10330773
Publication No. US20060040262A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: 529452001300
CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT FILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 981
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 772
LENGTH: 75782
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(75782)
OTHER INFORMATION: n = A,T,C or G
US-10-330-773-772

Query Match 2.6%; Score 21; DB 7; Length 75782;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 783 TCCTCTCCCTCTCCCTCTC 803
Db 22976 TCCTCTCCCTCTCCCTCTC 22956

RESULT 8
US-10-330-773-937/c
Sequence 937, Application US/10330773
Publication No. US20060040262A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
TITLE OF INVENTION: Novel Compositions and Methods in Cancer

FILE REFERENCE: 529452001300
CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT FILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 981
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 937
LENGTH: 390183
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(390183)
OTHER INFORMATION: n = A,T,C or G
US-10-330-773-937

Query Match 2.6%; Score 21; DB 7; Length 390183;
Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 784 CTCCTCTCCCTCTCCCTCTCC 804
Db 132970 CTCCTCTCCCTCTCCCTCTCC 132950

RESULT 9
US-10-995-561-13346
Sequence 13346, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13346
LENGTH: 43103
TYPE: DNA
ORGANISM: Homo sapiens
US-10-995-561-13346

Query Match 2.4%; Score 20; DB 8; Length 43103;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 785 TCCTCTCCCTCTCCCTCTCC 804
Db 37839 TCCTCTCCCTCTCCCTCTCC 37858

RESULT 10
US-10-330-773-416/c
Sequence 416, Application US/10330773
Publication No. US20060040262A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: 529452001300
CURRENT APPLICATION NUMBER: US/10/330,773
CURRENT FILING DATE: 2002-12-27
NUMBER OF SEQ ID NOS: 981
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 416
LENGTH: 71207
TYPE: DNA
ORGANISM: Homo sapiens
US-10-330-773-416

Query Match 2.4%; Score 20; DB 7; Length 71207;

Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 785 TCCTCTCCCTCTCCCTCTCC 804
DB 37377 TCCTCTCCCTCTCCCTCTCC 37358

RESULT 11
US-11-124-367A-5048/c
; Sequence 5048, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5048
; LENGTH: 100000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-5048

Query Match 2.4%; Score 20; DB 12; Length 100000;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 786 CCTCTCCCTCTCCCTCTCCG 805
DB 46014 CCTCTCCCTCTCCCTCTCCG 45995

RESULT 12
US-10-933-025-24/c
; Sequence 24, Application US/10933025
; Publication No. US20050265987A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN, STEVEN
; APPLICANT: HEMMERICH, STEFAN
; APPLICANT: TOMITA, MEGUMI
; TITLE OF INVENTION: Sulfotransferases and methods of use
; TITLE OF INVENTION: thereof
; FILE REFERENCE: UCAL-230CON
; CURRENT APPLICATION NUMBER: US/10/933,025
; CURRENT FILING DATE: 2004-09-01
; PRIOR APPLICATION NUMBER: 10/025,966
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/258,577
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: 60/267,831
; PRIOR FILING DATE: 2001-09-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 171936
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-933-025-24

Query Match 2.4%; Score 20; DB 8; Length 171936;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 785 TCCTCTCCCTCTCCCTCTCC 804
DB 33 TCCTCTCCCTCTCCCTCTCC 14

RESULT 13
US-10-330-773-395/c
; Sequence 395, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 395
; LENGTH: 194186
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(194186)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-395

Query Match 2.4%; Score 20; DB 7; Length 194186;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 785 TCCTCTCCCTCTCCCTCTCC 804
DB 99078 TCCTCTCCCTCTCCCTCTCC 99059

RESULT 14
US-10-310-914A-1382480/c
; Sequence 1382480, Application US/10310914A
; Publication No. US20060003322A1
; GENERAL INFORMATION:
; APPLICANT: Bentwich, Isaac
; APPLICANT: Shiller, Kuzat
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and
; TITLE OF INVENTION: uses thereof
; FILE REFERENCE: 06087.0200.CFUS01
; CURRENT APPLICATION NUMBER: US/10/310,914A
; CURRENT FILING DATE: 2002-12-06
; NUMBER OF SEQ ID NOS: 1388402
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1382480
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Human
US-10-310-914A-1382480

Query Match 2.3%; Score 19; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 786 CCTCTCCCTCTCCCTCTCC 804
DB 22 CCTCTCCCTCTCCCTCTCC 4

RESULT 15
US-10-995-561-17794
; Sequence 17794, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.

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; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17794
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-17794

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Query Match      2.3%; Score 19; DB 8; Length 201;
Best Local Similarity 100.0%; Pred.No. 6.3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 786 CCTCTCCCTCTCCCTCTCC 804
    |||||
Db 169 CCTCTCCCTCTCCCTCTCC 187

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Search completed: March 5, 2006, 11:44:32
Job time : 511 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 11:20:48 ; Search time 4129 Seconds
(without alignments)
9325.689 Million cell updates/sec

Title: US-10-660-208-90

Perfect score: 823

Sequence: 1 ctgacggtactccaagtat.....cgatccattctccagcgag 823

Scoring parameters: Gapop 60.0, Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST.*

- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_est3.*
- 4: gb_est4.*
- 5: gb_est5.*
- 6: gb_est6.*
- 7: gb_est7.*
- 8: gb_est8.*
- 9: gb_est9.*
- 10: gb_est10.*
- 11: gb_est11.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	473	57.5	901	10	CG011145
2	169	20.5	815	9	CC409846
3	125	15.2	964	9	CC331498
4	103	12.5	679	9	CC331420
5	103	12.5	894	9	CC356660
6	102	12.4	882	10	CG130321
7	102	12.4	1015	10	CG130320
8	97	11.8	893	10	CG2362236
9	85	10.3	324	9	CC007924
10	83	10.1	737	9	CC409551
11	80	9.7	563	2	BE510330
12	79	9.6	695	10	CW007582
13	79	9.6	777	10	CW006373
14	79	9.6	902	9	CC334197
15	79	9.6	902	9	CC607552
16	76	9.2	847	10	CW009430
17	76	9.2	863	10	CG175756
18	75	9.1	291	6	CF008956
19	75	9.1	534	6	CF010755
20	74	9.0	236	5	BU098918
21	70	8.5	530	6	CF008799
22	70	8.5	649	6	CF011104

23	69	8.4	560	2	BE644379	BE644379	946060P06
24	68	8.3	587	9	CC033608	CC033608	3591_1_64
25	68	8.3	595	9	CC033463	CC033463	3591_1_64
26	67	8.1	294	5	BU097711	BU097711	3524_1_45
27	67	8.1	558	6	CA826767	CA826767	1114004F0
28	67	8.1	606	1	AW499193	AW499193	660043F05
29	67	8.1	612	5	BO485904	BO485904	3524_1_9
30	67	8.1	905	10	CG065264	CG065264	PUPF072TD
31	65	7.9	617	1	AW428651	AW428651	660040H05
32	65	7.9	868	9	BZ817311	BZ817311	PUGCL66TD
33	65	7.9	985	9	BZ817308	BZ817308	PUGCL66TD
34	64	7.8	311	10	CL262067	CL262067	ZMWBB061
35	64	7.8	520	5	BQ528252	BQ528252	3524_1_2
36	64	7.8	530	5	BQ528654	BQ528654	3524_1_35
37	64	7.8	534	5	BQ577582	BQ577582	3524_1_38
38	64	7.8	574	5	BQ528264	BQ528264	3524_1_2
39	64	7.8	588	1	AW499212	AW499212	660043H02
40	64	7.8	611	5	BQ577641	BQ577641	3524_1_39
41	63	7.7	532	5	BU099109	BU099109	3524_1_3
42	63	7.7	544	1	AI833884	AI833884	605096G02
43	63	7.7	635	10	CG119014	CG119014	PUBB49TB
44	63	7.7	640	1	AW497918	AW497918	660041G02
45	63	7.7	717	9	CC397968	CC397968	PURDC37TD

ALIGNMENTS

RESULT 1
CG011145
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
ORIGIN
Query Match
Best Local Similarity
Matches 473; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 351 TTAGACTGATGCAGCTGCATTTCATAGACAAAACAGTGTAGAGCCGTATAGCAT 410


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CC331420
LOCUS       CC331420               679 bp    DNA          linear      GSS 16-MAY-2003
DEFINITION  OGMK41TV ZM_0.7.1.5_KB Zea mays genomic clone ZMMBMA0384G09,
genomic survey sequence.
ACCESSION   CC331420
VERSION     CC331420.1   GI:30800591
KEYWORDS    Zea mays
SOURCE      Zea mays
ORGANISM    Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 679)
AUTHORS     Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
            Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
            Consortium for Maize Genomics
            Unpublished (2002)
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: methylation filtered.
            Location/Qualifiers
                source          1..679
                /organism="Zea mays"
                /mol_type="genomic DNA"
                /strain="B73"
                /db_xref="taxon:4577"
                /clone="ZMMBMA0384G09"
                /note="Vector: pBSK-; Site 1: HincII; 0.7-1.5 kb
                methylation filtered genomic DNA library"

ORIGIN
Query Match      12.5%; Score 103; DB 9; Length 679;
Best Local Similarity 100.0%; Pred. No. 2.2e-45;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 143 CGAATATAGAGCTAAGACACTGTCTTCGTCAGATACATGCTTCGAGATTTTACAT 202
      |||||||
Db 260 CGAATATAGAGCTAAGACACTGTCTTCGTCAGATACATGCTTCGAGATTTTACAT 319

Cy 203 TCACCCCTAGACACACTCTTAAGACACAACTTAAGACACCCA 245
      |||||||
Db 320 TCACCCCTAGACACACTCTTAAGACACAACTTAAGACACCCA 362

RESULT 5
CC356660/c
LOCUS       CC356660               894 bp    DNA          linear      GSS 16-MAY-2003
DEFINITION  PUHQ61TD ZM_0.6.1.0_KB Zea mays genomic clone ZMMBTA513L02,
genomic survey sequence.
ACCESSION   CC356660
VERSION     CC356660.1   GI:30826060
KEYWORDS    Zea mays
SOURCE      Zea mays
ORGANISM    Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
            1 (bases 1 to 894)
            Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
            Maize Genomics Consortium
            Unpublished (2003)
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA

Query Match      12.5%; Score 103; DB 9; Length 679;
Best Local Similarity 100.0%; Pred. No. 2.2e-45;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 143 CGAATATAGAGCTAAGACACTGTCTTCGTCAGATACATGCTTCGAGATTTTACAT 202
      |||||||
Db 260 CGAATATAGAGCTAAGACACTGTCTTCGTCAGATACATGCTTCGAGATTTTACAT 319

Cy 203 TCACCCCTAGACACACTCTTAAGACACAACTTAAGACACCCA 245
      |||||||
Db 320 TCACCCCTAGACACACTCTTAAGACACAACTTAAGACACCCA 362

RESULT 5
CC356660/c
LOCUS       CC356660               894 bp    DNA          linear      GSS 16-MAY-2003
DEFINITION  PUHQ61TD ZM_0.6.1.0_KB Zea mays genomic clone ZMMBTA513L02,
genomic survey sequence.
ACCESSION   CC356660
VERSION     CC356660.1   GI:30826060
KEYWORDS    Zea mays
SOURCE      Zea mays
ORGANISM    Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
            1 (bases 1 to 894)
            Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
            Maize Genomics Consortium
            Unpublished (2003)
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
```

```
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
    source          1..894
    /organism="Zea mays"
    /mol_type="genomic DNA"
    /strain="B73"
    /db_xref="taxon:4577"
    /clone="ZMMBTA513L02"
    /note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
    Cot selected genomic DNA library"

ORIGIN
Query Match      12.5%; Score 103; DB 9; Length 894;
Best Local Similarity 100.0%; Pred. No. 2.2e-45;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 143 CGAATATAGAGCTAAGACACTGTCTTCGTCAGATACATGCTTCGAGATTTTACAT 202
      |||||||
Db 131 CGAATATAGAGCTAAGACACTGTCTTCGTCAGATACATGCTTCGAGATTTTACAT 72

Cy 203 TCACCCCTAGACACACTCTTAAGACACAACTTAAGACACCCA 245
      |||||||
Db 71 TCACCCCTAGACACACTCTTAAGACACAACTTAAGACACCCA 29

RESULT 6
CG130321
LOCUS       CG130321               882 bp    DNA          linear      GSS 21-AUG-2003
DEFINITION  PUKDM45TD ZM_0.6.1.0_KB Zea mays genomic clone ZMMBTA0794H17,
genomic survey sequence.
ACCESSION   CG130321
VERSION     CG130321.1   GI:34017768
KEYWORDS    Zea mays
SOURCE      Zea mays
ORGANISM    Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
            1 (bases 1 to 882)
            Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
            Bennetzen,J.
            Maize Genomics Consortium
            Unpublished (2003)
            Other GSSs: PUKDM45TB
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: sheared ends.
            Location/Qualifiers
                source          1..882
                /organism="Zea mays"
                /mol_type="genomic DNA"
                /strain="B73"
                /db_xref="taxon:4577"
                /clone="ZMMBTA0794H17"
                /note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
                Cot selected genomic DNA library"

ORIGIN
Query Match      12.4%; Score 102; DB 10; Length 882;
Best Local Similarity 100.0%; Pred. No. 7.9e-45;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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144 GAATATAGAGCTAAGACACTGTGCTTCGTCAGATACATGCTTGAGATTTTACATT 203
Db |||||||
578 GAATATAGAGCTAAGACACTGTGCTTCGTCAGATACATGCTTGAGATTTTACATT 637
Qy |||||||
204 CACCCCCCTAGACACACTCTTAAGACACAACTTTAAGACACCCA 245
Db |||||||
638 CACCCCCCTAGACACACTCTTAAGACACAACTTTAAGACACCCA 679

RESULT 7
CGI30320/c 1015 bp DNA linear GSS 21-AUG-2003
LOCUS FUKDM45TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0794H17,
DEFINITION genomic survey sequence.
ACCESSION CGI30320
VERSION CGI30320.1 GI:34017767
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1015)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
Maize Genomics Consortium
TITLE Unpublished (2003)
JOURNAL PUKDM45TDP
COMMENT Other_GSSs: FUKDM45TDP
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.

FEATURES
source
1..1015
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone_lib="ZMMBTa0794H17"
/clone_lib="ZM_0.6_1.0_KB"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
Cot selected genomic DNA library"

ORIGIN
Query Match 12.4%; Score 102; DB 10; Length 1015;
Best Local Similarity 100.0%; Pred. No. 7.9e-45;
Matches 102; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 144 GAATATAGAGCTAAGACACTGTGCTTCGTCAGATACATGCTTGAGATTTTACATT 203
Db |||||||
849 GAATATAGAGCTAAGACACTGTGCTTCGTCAGATACATGCTTGAGATTTTACATT 790

Qy 204 CACCCCCCTAGACACACTCTTAAGACACAACTTTAAGACACCCA 245
Db |||||||
789 CACCCCCCTAGACACACTCTTAAGACACAACTTTAAGACACCCA 748

RESULT 8
CZ362236/c 893 bp DNA linear GSS 29-MAR-2005
LOCUS ZMMBF0140018r ZMMBF Zea mays genomic clone ZMMBF0140018.3, genomic
DEFINITION survey sequence.
ACCESSION CZ362236
VERSION CZ362236.1 GI:61972180
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 893)
AUTHORS Bharti,A.K., Nelson,A.B., Young,S., Keizer,G., Zohovetz,V., Fuks,G.
and Messing,J.
Construction, Sequencing and Characterization of a Fosmid Library
of the B73 Maize Genome
Unpublished (2005)
CONTACT: Bharti,A.K.
Dr. Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: SP6
Class: fosmid ends.

FEATURES
source
1..893
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBF0140018"
/lab_host="EPI100-T1"
/clone_lib="ZMMBF"
/note="vector: pEpiFOS-5; Site_1: Eco72I"

ORIGIN
Query Match 11.8%; Score 97; DB 10; Length 893;
Best Local Similarity 100.0%; Pred. No. 4.8e-42;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 143 CGAATATAGAGCTAAGACACTGTGCTTCGTCAGATACATGCTTGAGATTTTACAT 202
Db |||||||
307 CGAATATAGAGCTAAGACACTGTGCTTCGTCAGATACATGCTTGAGATTTTACAT 248

Qy 203 TCACCCCTAGACACACTCTTAAGACACAACTTAAGA 239
Db |||||||
247 TCACCCCTAGACACACTCTTAAGACACAACTTAAGA 211

RESULT 9
CC007924 324 bp DNA linear GSS 31-MAR-2003
LOCUS PUBE148TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa197H23,
DEFINITION genomic survey sequence.
ACCESSION CC007924
VERSION CC007924.1 GI:293866487
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 324)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
Maize Genomics Consortium
TITLE Unpublished (2003)
JOURNAL Contact: Cathy Whitelaw
COMMENT TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
Class: sheared ends.

FEATURES
source
1..324
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone_lib="ZMMBTa197H23"
/clone_lib="ZM_0.6_1.0_KB"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
Cot selected genomic DNA library"

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/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone_lib="ZM 0.6 1.0 KB"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
Cot selected genomic DNA library"

ORIGIN

Query Match      10.3%; Score 85; DB 9; Length 324;
Best Local Similarity 100.0%; Pred. No. 2.3e-35;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 ACTGTGCTTCGTCAGATACATGCTTGTGAGATTTTACATTCACCCCTAGACAC 220
Db 30 ACTGTGCTTCGTCAGATACATGCTTGTGAGATTTTACATTCACCCCTAGACAC 89

QY 221 TCTAAGACACAACTTAAGACACCA 245
Db 90 TCTAAGACACAACTTAAGACACCA 114

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```

RESULT 10
CC409551/c
LOCUS      737 bp      DNA      linear      GSS 19-MAY-2003
DEFINITION genomic survey sequence.
ACCESSION  CC409551
VERSION    CC409551.1 GI:30889641
KEYWORDS   GSS.
SOURCE     Zea mays
ORGANISM   Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 737)
AUTHORS   Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
          Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
          Bennetzen,J.
TITLE     Maize Genomics Consortium
JOURNAL   Unpublished (2003)
COMMENT   Contact: Cathy Whitelaw
          TIGR
          9712 Medical Center Drive, Rockville, MD 20850, USA
          Tel: 301-838-5843
          Fax: 301-838-0208
          Email: whitelaw@tigr.org
          Seq primer: TF
          Class: sheared ends.
FEATURES   Location/Qualifiers
            source          1..737
                        /organism="Zea mays"
                        /mol_type="genomic DNA"
                        /strain="B73"
                        /db_xref="taxon:4577"
                        /clone_lib="ZM 0.6 1.0 KB"
                        /notes="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
                        Cot selected genomic DNA library"

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ORIGIN

Query Match      10.1%; Score 83; DB 9; Length 737;
Best Local Similarity 100.0%; Pred. No. 3.1e-34;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 163 TGTGCTTCGTCAGATACATGCTTGTGAGATTTTACATTCACCCCTAGACAC 222
Db 146 TGTGCTTCGTCAGATACATGCTTGTGAGATTTTACATTCACCCCTAGACAC 87

QY 223 TAAGACACAACTTAAGACACCA 245
Db 86 TAAGACACAACTTAAGACACCA 64

```

```

RESULT 11
BE510330
LOCUS      563 bp      mRNA      linear      EST 07-AUG-2000
DEFINITION 946052B01.x1 946 - tassels primordium prepared by Schmidt lab Zea
          mays cDNA, mRNA sequence.
ACCESSION  BE510330
VERSION    BE510330.1 GI:9731578
KEYWORDS   EST.
SOURCE     Zea mays
ORGANISM   Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 563)
AUTHORS   Walbot,V.
TITLE     Maize ESTs from various cDNA libraries sequenced at Stanford
          University
JOURNAL   Unpublished (1999)
COMMENT   Contact: Walbot V
          Department of Biological Sciences
          Stanford University
          855 California Ave, Palo Alto, CA 94304, USA
          Tel: 650 723 2227
          Fax: 650 725 8221
          Email: walbot@stanford.edu
          Plate: 946052 row: B column: 01.
FEATURES   Location/Qualifiers
            source          1..563
                        /organism="Zea mays"
                        /mol_type="mRNA"
                        /cultivar="OH43"
                        /db_xref="taxon:4577"
                        /tissue_type="tassels"
                        /dev_stage="just after the transition from vegetative to
                        inflorescence development"
                        /lab_host="XLOLR"
                        /clone_lib="946 - tassels primordium prepared by Schmidt
                        lab"

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ORIGIN

Query Match      9.7%; Score 80; DB 2; Length 563;
Best Local Similarity 100.0%; Pred. No. 1.4e-32;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 160 CACTGTGCTTCGTCAGATACATGCTTGTGAGATTTTACATTCACCCCTAGACACA 219
Db 1 CACTGTGCTTCGTCAGATACATGCTTGTGAGATTTTACATTCACCCCTAGACACA 60

QY 220 CTTCAAGACACAACTTAAGA 239
Db 61 CTTCAAGACACAACTTAAGA 80

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RESULT 12
CW007582
LOCUS      695 bp      DNA      linear      GSS 23-SEP-2004
DEFINITION ZM5BLA0009E11.r ZM5BLA Zea mays genomic clone ZM5BLA0009E11 3',
          genomic survey sequence.
ACCESSION  CW007582
VERSION    CW007582.1 GI:52588391
KEYWORDS   GSS.
SOURCE     Zea mays
ORGANISM   Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

```


REFERENCE	1 (bases 1 to 695)
AUTHORS	Wing, R., Luo, M., Soderlund, C. and Haller, K.
TITLE	ZMMBL sequences
JOURNAL	Unpublished (2004)
COMMENT	Contact: Rod A. Wing Arizona Genomics Institute University of Arizona Forbes Building Room 303, Tucson, AZ 85721-0036, USA Tel: 520 626 9595 Fax: 520 621 1259 Email: rwing@genome.arizona.edu Plate: 0009 row: E column: 11 Class: BAC ends.

	/note_ vector: prg(ancez) state_ gain_ loss_
ORIGIN	
Query Match	9.6%; Score 79; DB 10; Length 695;
Best Local Similarity	100.0%; Pred. No. 5.2e-32;
Matches	79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	143 CGAATATAGAGCTTAAGACACTGTGTCCTTGGTCAAGATACATGCTCTTGAGATTTTTTACAT 202
Dd	398 CGAATATAGAGCTTAAGACACTGTGTCCTTGGTCAAGATACATGCTCTTGAGATTTTTTACAT 457
Qy	203 TCACCCGCCCTTAGACACACT 221
Dd	458 TCACCCGCCCTTAGACACACT 476

RESULT	13
CW006373	
LOCUS	ZMMLA0007D24.f ZMMLA Zea mays genomic clone ZMMLA0007D24 5', linear GSS 23-SEP-2004
DEFINITION	genomic survey sequence.
ACCESSION	CW006373
VERSION	CW006373.1 GI:52585956
KEYWORDS	GSS.
SOURCE	Zea mays
ORGANISM	Zea mays
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
AUTHORS	1. (bases 1 to 777)
TITLE	Wing, R., Luo, M., Soderlund, C. and Haller, K.
JOURNAL	ZMML sequences
COMMENT	Unpublished (2004) Contact: Rod A. Wing

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Class: SAC_endon/Qualifiers
location/Qualifiers
    777
    /organism="Zea mays"
    /mol_type="genomic DNA"
    /cultivar="B73"
    /db_xref="taxon:4577"
    /clone="ZMMLa0007D24"
    /tissue_type="immature ears"

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ORIGIN

	Query Match	9.6%	Score 79	DB 10	Length 777	
	Best Local Similarity	100.0%	Pred No. 5.2e-32			
	Matches	79	Conservative	0	Mismatches	0
					Indels	Gaps
QY	143	CGAATATAGAGCTTAAGACACTGTGTCTTCGTCAAGATACATGCTCTTGAGATT	TTTTTACAT	202		
Db	405	CGAATATAGAGCTTAAGACACTGTGTCTTCGTCAAGATACATGCTCTTGAGATT	TTTTTACAT	464		
QY	203	TCACCCCCCTTAGACACACT	221			
Db	465	TCACCCCCCTTAGACACACT	483			

RESULT	14
CC334197/c	
LOCUS	GSS 16-MAY-2003 linear
DEFINITION	OgURNB60TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMEMa040LJ24,
ACCESSION	CC334197
VERSION	CC334197
KEYWORDS	GSS.
SOURCE	Zea mays
ORGANISM	Zea mays
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 902)
TITLE	Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.F.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
JOURNAL COMMENT	Consortium for Maize Genomes Unpublished (2002) Contact: Cathv Whitelaw

FEATURES
SOURCE

ORIGIN

Query Match .	9.6%	Score 79;	DB 9;	Length 902;
Best Local Similarity	100.0%;	Pred. No. 5.2e-32;		
Matches	79;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0
QY	143	CGAATATAGAGCTTAAGACACTGTGTCCTTCGTCGAAGATACATGTCCTTGAGATTTTACAT	202	
Db	886	CGAATATAGAGCTTAAGACACTGTGTCCTTCGTCGAAGATACATGTCCTTGAGATTTTACAT	827	
QY	203	TCACCCCCCTTAGACACACT	221	
Db	826	TCACCCCCCTTAGACACACT	808	

RESULT 15				
CC607552				
LOCUS				
CC607552	902 bp	DNA	linear	GSS 18-JUN-2003

DEFINITION OGUEN60TV ZM_0.7.1.5 KB Zea mays genomic clone ZMMBMA0401J24,
genomic survey sequence.
ACCESSION CC607552
VERSION CC607552.1 GI:31968973
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 902)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Reanick,A., Frazer,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
TITLE Unpublished (2002)
JOURNAL Other GSSs: OGUEN60TH
COMMENT Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: methylation filtered.
FEATURES
source
1..902
Location/Qualifiers
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0401J24"
/clone_lib="ZM_0.7.1.5_KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
ORIGIN
Query Match 9.6%; Score 79; DB 9; Length 902;
Best Local Similarity 100.0%; Pred. No. 5.2e-32;
Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 143 CGAATATAGACTAAGACACTGTGTTCTTCGTCGAAGATACATGCTTCGAGATTTTTCAT 202
|||||
Db 503 CGAATATAGACTAAGACACTGTGTTCTTCGTCGAAGATACATGCTTCGAGATTTTTCAT 562
|||||
Qy 203 TCACCCCTTAGACACT 221
|||||
Db 563 TCACCCCTTAGACACT 581
|||||

Search completed: March 5, 2006, 14:56:37
Job time : 4131 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 08:22:14 ; Search time 878 Seconds
(without alignments)
1666.211 Million cell updates/sec

Title: US-10-660-208-90

Perfect score: 823

Sequence: 1 ctccacgctactccaagtat.....cgatcccttcctccagcag 823

Scoring table: Q8F6C-NUC

Gapop 60.0, Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size: 6

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq:*
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq:*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	36	4.4	6343	3	US-08-581-148C-30
2	32	3.9	6550	3	US-09-037-319A-1
3	32	3.9	6550	3	US-09-037-319A-1
4	32	3.9	9299	3	US-09-037-319A-15
5	32	3.9	9299	3	US-09-037-319A-15
6	32	3.9	9408	3	US-09-037-319A-16
7	32	3.9	9408	3	US-09-037-319A-16
8	30	3.6	720	3	US-09-950-933A-8
9	22	2.7	173787	3	US-09-949-016-12542
10	22	2.7	173791	3	US-09-949-016-17302
11	21	2.6	601	3	US-09-949-016-53357
12	21	2.6	37385	3	US-09-949-016-15354
13	21	2.6	95648	3	US-09-949-016-13139
14	21	2.6	102053	3	US-09-949-016-13025
15	21	2.6	133613	3	US-09-949-016-15824
16	21	2.6	139936	3	US-09-949-016-11782
17	21	2.6	139952	3	US-09-949-016-13280
18	21	2.6	193169	3	US-09-949-016-15091
19	21	2.6	236474	3	US-09-949-016-13418
20	20	2.4	154	3	US-09-313-294A-6978
21	20	2.4	601	3	US-09-949-016-87134
22	20	2.4	601	3	US-09-949-016-197000
23	20	2.4	601	3	US-09-949-016-197001
24	20	2.4	601	3	US-09-949-016-197002

c 25	20	2.4	601	3	US-09-949-016-197003	Sequence 197003, A
c 26	20	2.4	8764	3	US-09-949-016-17326	Sequence 17326, A
c 27	20	2.4	33769	3	US-09-544-398B-8	Sequence 8, Appli
c 28	20	2.4	33769	3	US-09-544-398B-8	Sequence 8, Appli
c 29	20	2.4	34414	3	US-09-949-016-12330	Sequence 12330, A
c 30	20	2.4	34414	3	US-09-949-016-16157	Sequence 16157, A
c 31	20	2.4	35256	3	US-09-949-016-11991	Sequence 11991, A
c 32	20	2.4	43717	3	US-09-949-016-16821	Sequence 16821, A
c 33	20	2.4	59948	3	US-09-949-016-15594	Sequence 15594, A
c 34	20	2.4	83938	3	US-09-949-016-16068	Sequence 16068, A
c 35	20	2.4	140844	3	US-09-949-016-14199	Sequence 14199, A
c 36	20	2.4	168174	3	US-10-071-411A-63	Sequence 63, Appli
c 37	20	2.4	168273	3	US-10-071-411A-2	Sequence 2, Appli
c 38	19	2.3	343	3	US-09-640-211A-109	Sequence 109, App
c 39	19	2.3	380	3	US-09-640-211A-1501	Sequence 1501, Ap
c 40	19	2.3	601	3	US-09-949-016-21808	Sequence 21808, A
c 41	19	2.3	601	3	US-09-949-016-21809	Sequence 21809, A
c 42	19	2.3	601	3	US-09-949-016-41156	Sequence 41156, A
c 43	19	2.3	601	3	US-09-949-016-41157	Sequence 41157, A
c 44	19	2.3	601	3	US-09-949-016-64813	Sequence 64813, A
c 45	19	2.3	601	3	US-09-949-016-81824	Sequence 81824, A

ALIGNMENTS

RESULT 1
US-08-581-148C-30
; Sequence 30, Application US/08581148C
; Patent No. 6060644
; GENERAL INFORMATION:
; APPLICANT: Schnable, Patrick S.
; APPLICANT: Robertson, Donald S.
; APPLICANT: Hansen, Joel D.
; APPLICANT: Nikolau, Basil J.
; APPLICANT: Xu, Xiaojie
; APPLICANT: Xia, Yiji
; TITLE OF INVENTION: ISOLATION AND USE OF CUTICULAR LIPID
; TITLE OF INVENTION: GENES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: Two Prudential Plaza, Suite 4900
; CITY: Chicago
; STATE: IL
; COUNTRY: US
; ZIP: 60601-6780
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/581,148C
; FILING DATE: 29-DEC-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Larcher, Carol
; REGISTRATION NUMBER: 35243
; REFERENCE/DOCKET NUMBER: 71380
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6343 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Zea mays
; INDIVIDUAL ISOLATE: Z.mays Glossy2 locus DNA

US-08-581-148C-30

Query Match 4.4%; Score 36; DB 3; Length 6343;
Best Local Similarity 100.0%; Pred. No. 3.9e-09;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 CATTCAATAAATTAAGTGACCAATCAGATAGTCCTC 136
Db 3715 CATTCAATAAATTAAGTGACCAATCAGATAGTCCTC 3750

RESULT 2

US-09-097-319A-1

; Sequence 1, Application US/09097319A

; Patent No. 6384207

; GENERAL INFORMATION:

; APPLICANT: Ainley, Michael

; APPLICANT: Armstrong, Katherine

; APPLICANT: Belmar, Scott

; APPLICANT: Folkerts, Otto

; APPLICANT: Hopkins, Nicole

; APPLICANT: Menke, Michael A.

; APPLICANT: Paredy, Davakar

; APPLICANT: Petolino, Joseph F.

; APPLICANT: Smith, Kelley

; APPLICANT: Woosley, Aaron

; TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DowElanco Patent Department

; STREET: 9330 Zionsville Road

; CITY: Indianapolis

; STATE: Indiana

; COUNTRY: USA

; ZIP: 46268

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/097,319A

; FILING DATE:

; CLASSIFICATION: 800

; ATTORNEY/AGENT INFORMATION:

; NAME: Stuart, Donald R

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 317 337 4816

; TELEFAX: 317 337 4847

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6550 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

; FEATURE:

; NAME/KEY: exon

; LOCATION: 4201..4425

; OTHER INFORMATION: /product= "Peroxidase"

; FEATURE:

; NAME/KEY: intron

; LOCATION: 4426..5058

; FEATURE:

; NAME/KEY: exon

; LOCATION: 5059..5250

; FEATURE:

; NAME/KEY: intron

; LOCATION: 5251..5382

; FEATURE:

; NAME/KEY: exon

; LOCATION: 5383..5548

; FEATURE:

; NAME/KEY: intron

; LOCATION: 5549..5649

; FEATURE:

; NAME/KEY: exon

; LOCATION: 5650..6065

; FEATURE:

; NAME/KEY: CDS

; LOCATION: join(4201..4425, 5059..5250, 5383..5547, 5649

; LOCATION: ..6068)

; US-09-097-319A-1

Query Match 3.9%; Score 32; DB 3; Length 6550;

Best Local Similarity 100.0%; Pred. No. 5.9e-07;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 TCTAAACATGTGCTTACCATTTCATTGTA 90

Db 1415 TCTAAACATGTGCTTACCATTTCATTGTA 1446

RESULT 3

US-09-643-971-1

; Sequence 1, Application US/09643971

; Patent No. 6699984

; GENERAL INFORMATION:

; APPLICANT: Ainley, Michael

; APPLICANT: Armstrong, Katherine

; APPLICANT: Belmar, Scott

; APPLICANT: Folkerts, Otto

; APPLICANT: Hopkins, Nicole

; APPLICANT: Menke, Michael A.

; APPLICANT: Paredy, Davakar

; APPLICANT: Petolino, Joseph F.

; APPLICANT: Smith, Kelley

; APPLICANT: Woosley, Aaron

; TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DowElanco Patent Department

; STREET: 9330 Zionsville Road

; CITY: Indianapolis

; STATE: Indiana

; COUNTRY: USA

; ZIP: 46268

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/643,971

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Stuart, Donald R

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 317 337 4816

; TELEFAX: 317 337 4847

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6550 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

; FEATURE:

; NAME/KEY: exon

; LOCATION: 4201..4425

; OTHER INFORMATION: /product= "Peroxidase"

; FEATURE:

; NAME/KEY: intron

; LOCATION: 4426..5058

; FEATURE:

NAME/KEY: exon
LOCATION: 5059..5250
FEATURE:
NAME/KEY: intron
LOCATION: 5251..5382
FEATURE:
NAME/KEY: exon
LOCATION: 5383..5548
FEATURE:
NAME/KEY: intron
LOCATION: 5549..5649
FEATURE:
NAME/KEY: exon
LOCATION: 5650..6065
FEATURE:
NAME/KEY: CDS
LOCATION: join(4201..4425, 5059..5250, 5383..5547, 5649
LOCATION: ..6068)
US-09-643-971-1

Query Match 3.9%; Score 32; DB 3; Length 6550;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 TCTAAACATGTGCTTACCATTTCATTGTA 90
|||||
Db 1415 TCTAAACATGTGCTTACCATTTCATTGTA 1446

RESULT 4
US-09-097-319A-15
; Sequence 15, Application US/09097319A
; Patent No. 6384207
; GENERAL INFORMATION:
; APPLICANT: Ainley, Michael
; APPLICANT: Armstrong, Katherine
; APPLICANT: Belmar, Scott
; APPLICANT: Folkerts, Otto
; APPLICANT: Hopkins, Nicole
; APPLICANT: Menke, Michael A.
; APPLICANT: Paredy, Dayakar
; APPLICANT: Petolino, Joseph F.
; APPLICANT: Smith, Kelley
; APPLICANT: Woosley, Aaron
; TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dowelanco Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/097,319A
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stuart, Donald R
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317 337 4816
; TELEFAX: 317 337 4847
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9299 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular

MOLECULE TYPE: DNA
US-09-097-319A-15
Query Match 3.9%; Score 32; DB 3; Length 9299;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 59 TCTAAACATGTGCTTACCATTTCATTGTA 90
|||||
Db 1462 TCTAAACATGTGCTTACCATTTCATTGTA 1493
RESULT 5
US-09-643-971-15
; Sequence 15, Application US/09643971
; Patent No. 6699984
; GENERAL INFORMATION:
; APPLICANT: Ainley, Michael
; APPLICANT: Armstrong, Katherine
; APPLICANT: Belmar, Scott
; APPLICANT: Folkerts, Otto
; APPLICANT: Hopkins, Nicole
; APPLICANT: Menke, Michael A.
; APPLICANT: Paredy, Dayakar
; APPLICANT: Petolino, Joseph F.
; APPLICANT: Smith, Kelley
; APPLICANT: Woosley, Aaron
; TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dowelanco Patent Department
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/643,971
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stuart, Donald R
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317 337 4816
; TELEFAX: 317 337 4847
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9299 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA
US-09-643-971-15
Query Match 3.9%; Score 32; DB 3; Length 9299;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 59 TCTAAACATGTGCTTACCATTTCATTGTA 90
|||||
Db 1462 TCTAAACATGTGCTTACCATTTCATTGTA 1493
RESULT 6
US-09-097-319A-16
; Sequence 16, Application US/09097319A
; Patent No. 6384207
; GENERAL INFORMATION:

APPLICANT: Ainley, Michael
APPLICANT: Armstrong, Katherine
APPLICANT: Belmar, Scott
APPLICANT: Folkerts, Otto
APPLICANT: Hopkins, Nicole
APPLICANT: Menke, Michael A.
APPLICANT: Paredy, Dayakar F.
APPLICANT: Petolino, Joseph F.
APPLICANT: Smith, Kelley
APPLICANT: Woosley, Aaron
TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dowelanco Patent Department
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,319A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317 337 4816
TELEFAX: 317 337 4847
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 9408 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA
US-09-097-319A-16
Query Match 3.9%; Score 32; DB 3; Length 9408;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 59 TCTAAACATGTCCTTACCATTTCATTGTA 90
Db 1468 TCTAAACATGTCCTTACCATTTCATTGTA 1499
RESULT 7
US-09-643-971-16
Sequence 16, Application US/09643971
Patent No. 669984
GENERAL INFORMATION:
APPLICANT: Ainley, Michael
APPLICANT: Armstrong, Katherine
APPLICANT: Belmar, Scott
APPLICANT: Folkerts, Otto
APPLICANT: Hopkins, Nicole
APPLICANT: Menke, Michael A.
APPLICANT: Paredy, Dayakar F.
APPLICANT: Petolino, Joseph F.
APPLICANT: Smith, Kelley
APPLICANT: Woosley, Aaron
TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dowelanco Patent Department
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: Indiana

COUNTRY: USA
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,971
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317 337 4816
TELEFAX: 317 337 4847
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 9408 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA
US-09-643-971-16
Query Match 3.9%; Score 32; DB 3; Length 9408;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 59 TCTAAACATGTCCTTACCATTTCATTGTA 90
Db 1468 TCTAAACATGTCCTTACCATTTCATTGTA 1499
RESULT 8
US-09-950-933A-8
Sequence 8, Application US/09950933A
Patent No. 6875907
GENERAL INFORMATION:
APPLICANT: Simmons, Carl R.
APPLICANT: Navarro, Pedro
TITLE OF INVENTION: Antimicrobial Peptides and Methods of
TITLE OF INVENTION: Use
FILE REFERENCE: 35718/238472
CURRENT APPLICATION NUMBER: US/09/950,933A
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: 60/232,569
PRIOR FILING DATE: 2000-09-13
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 720
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: CDS
LOCATION: (119)....(403)
US-09-950-933A-8
Query Match 3.6%; Score 30; DB 3; Length 720;
Best Local Similarity 100.0%; Pred. No. 7e-06;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 48 CAGTGGTCATGTCCTAAACATGTCCTTAC 77
Db 625 CAGTGGTCATGTCCTAAACATGTCCTTAC 654
RESULT 9
US-09-949-016-12542/c
Sequence 12542, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12542
; LENGTH: 173787
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12542

Query Match 2.7%; Score 22; DB 3; Length 173787;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 783 TCTCTCTCCCTCTCCCTCTCC 804
Db 113387 TCTCTCTCCCTCTCCCTCTCC 113366

RESULT 10
US-09-949-016-17302/c
; Sequence 17302, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17302
; LENGTH: 173791
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17302

Query Match 2.7%; Score 22; DB 3; Length 173791;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 783 TCTCTCTCCCTCTCCCTCTCC 804
Db 113387 TCTCTCTCCCTCTCCCTCTCC 113366

RESULT 11
US-09-949-016-53357/c
; Sequence 53357, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12542
; LENGTH: 173787
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12542

; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53357
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-53357

Query Match 2.6%; Score 21; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 784 CTCTCTCCCTCTCCCTCTCC 804
Db 442 CTCTCTCCCTCTCCCTCTCC 422

RESULT 12
US-09-949-016-15354/c
; Sequence 15354, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15354
; LENGTH: 37385
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15354

Query Match 2.6%; Score 21; DB 3; Length 37385;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 784 CTCTCTCCCTCTCCCTCTCC 804
Db 9330 CTCTCTCCCTCTCCCTCTCC 9310

RESULT 13
US-09-949-016-13139/c
; Sequence 13139, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13139
; LENGTH: 13139
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13139

;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 13139
;; LENGTH: 95648
;; TYPE: DNA
;; ORGANISM: Human
;; NAME/KEY: misc feature
;; LOCATION: (1)...(95648)
;; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13139

Query Match 2.6%; Score 21; DB 3; Length 95648;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 784 CTCCTCTCCCTCTCCCTCTCC 804
Db 64354 CTCCTCTCCCTCTCCCTCTCC 64334

RESULT 14
US-09-949-016-13025/c
; Sequence 13025, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13025
; LENGTH: 102053
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(102053)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13025

Query Match 2.6%; Score 21; DB 3; Length 102053;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 784 CTCCTCTCCCTCTCCCTCTCC 804
Db 88871 CTCCTCTCCCTCTCCCTCTCC 88851

RESULT 15
US-09-949-016-15824/c
; Sequence 15824, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755

;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 15824
;; LENGTH: 133613
;; TYPE: DNA
;; ORGANISM: Human
;; NAME/KEY: misc feature
;; LOCATION: (1)...(133613)
;; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15824

Query Match 2.6%; Score 21; DB 3; Length 133613;
Best Local Similarity 100.0%; Pred. No. 0.58;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 784 CTCCTCTCCCTCTCCCTCTCC 804
Db 109203 CTCCTCTCCCTCTCCCTCTCC 109183

Search completed: March 5, 2006, 08:37:01
Job time : 880 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 11:12:37 ; Search time 557 Seconds
(without alignments) 9847.472 Million cell u

Title: US-10-660-208-90

Perfect score:

Sequence: 1 ctgcàgggtactccaagtat.....cgatccattctccagcgag 823

Scoring table: **COLTCONUC**
Gapop 60.0 : Gapext 60.0

Searched: 4996997 seqs, 332346308 residues

THE UNIVERSITY OF CHICAGO

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

- N_Geneseq_21:*
- | | |
|-----|------------------|
| 1: | Geneseqm1990s:* |
| 2: | Geneseqm1980s:* |
| 3: | Geneseqm2000s:* |
| 4: | Geneseqm2001s:* |
| 5: | Geneseqm2001bs:* |
| 6: | Geneseqm2002s:* |
| 7: | Geneseqm2002bs:* |
| 8: | Geneseqm2003s:* |
| 9: | Geneseqm2003bs:* |
| 10: | Geneseqm2003cs:* |
| 11: | Geneseqm2003ds:* |
| 12: | Geneseqm2004s:* |
| 13: | Geneseqm2004bs:* |
| 14: | Geneseqm2005s:* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	823	100.0	823	6	AAS96569	Aas96569 Corn prom
2	473	57.5	1587	6	AA598566	Aas98566 Corn prom
3	74	5.0	769	3	AAC43750	Aac43750 Zea mays
c 4	63	7.7	485	13	ADX49209	Adx49209 Plant full
5	62	7.5	821	13	ADX33652	Adx33652 Plant full
6	59	7.2	791	13	ADX30094	Adx30094 Plant full
7	59	7.2	795	13	ADX30071	Adx30071 Plant full
8	49	6.0	781	13	ADX33856	Adx33856 Plant full
9	40	4.9	307	6	ABL76691	Abl76691 Corn tass
10	40	4.9	1326	13	ADX60974	Adx60974 Plant full
11	36	4.4	782	13	ADX33827	Adx33827 Plant full
c 12	36	4.4	1578	13	ADX48086	Adx48086 plant full
13	36	4.4	6343	3	AAA57891	Aaa57891 Maize glo
14	32	3.9	6550	2	AAV63717	Aav63717 Maize per
15	32	3.9	9299	2	RAV63730	Rav63730 Vector pl
16	32	3.9	9408	2	AAV63731	Aav63731 Vector pl
17	30	3.6	720	6	AAI37816	Aai37816 Corn KCP-
18	30	3.6	737	13	ADX53136	Adx53136 Plant full
c 19	25	3.0	38	6	AAS96543	Aas96543 Primer #6

ALIGNMENTS

RESULT 1

AAS96569
ID AAS96569 standard: DNA; 823 BP.

AC AAS96569;

26-FEB-2002 (first entry)

DE Corn promoter sequence #12

Corn: male reproductive tis

KW promoter; transcription reg
wheat anther: plant fertili

KW herbicide tolerance; ds.
XX

OS Zea mays.
yy

PN : WO200183790-A2.

PD 08-NOV-2001:

PF 30-APR-2001; 2001WO-US01373

PR 01-MAY-2000; 2000US-0201255

PA (MONS) MONSANTO TECHNOLOGY

PI Conner TW, Dubois P, Malv

DR WPI; 2002-055481/07.

Novel promoters isolated from

male reproductive tissues, PT transcription of target genes

XX
Pt: tolerance.

PS Claim 1; page 113-114; 121p/

The present invention relates

CC promoter sequences, fragments

Db 1211 CAGAAGTATTGTGGCTCATATTCTGTAATTTATAGCGAGGGCCCAAGGCCCATCACTTC 1270
Qy 531 ACTTCGAGGTGAGCATTTGTTTGTAACTTCGATTAATTTGTTTCTACTTAAATAG 590
Db 1271 ACTTCGAGGTGAGCATTTGTTTGTAACTTCGATTAATTTGTTTCTACTTAAATAG 1330
Qy 591 ACCAGTTCAATTTCTGGTCTTAGTCAATGCTGGATCCAGGGGGAGCGAGAGCGAA 650
Db 1331 ACCAGTTCAATTTCTGGTCTTAGTCAATGCTGGATCCAGGGGGAGCGAGAGCGAA 1390
Qy 651 TGTGTGCCCCCGCAGTGGAGGCCAAGCCGAGCCCGTCTCGTCCGATCCAAACCCCCCTCG 710
Db 1391 TGTGTGCCCCCGCAGTGGAGGCCAAGCCGAGCCCGTCTCGTCCGATCCAAACCCCCCTCG 1450
Qy 711 TTTTACTATATATACACAGACGACGATACCCATATCGTGGTCTAGAGCAACTGAAA 770
Db 1451 TTTTACTATATATACACAGACGACGATACCCATATCGTGGTCTAGAGCAACTGAAA 1510
Qy 771 ACAGCGAGCGATCTCTCTCCCTCTCCCTCTCCGATCCATTTCTCCAGCGCAG 823
Db 1511 ACAGCGAGCGATCTCTCTCCCTCTCCCTCTCCGATCCATTTCTCCAGCGCAG 1563

RESULT 3

AAC43750
ID AAC43750 standard; DNA; 769 BP.

XX AAC43750;

XX 18-OCT-2000 (first entry)

XX Zea mays DNA fragment SEQ ID NO: 40373.

KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic; pathway;
KW promoter; termination sequence; corn; ss.

OS Zea mays subsp. mays.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125768P.

PR 25-MAR-1999; 99US-0126264P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.

PR 06-APR-1999; 99US-0128234P.

PR 08-APR-1999; 99US-0128714P.

PR 16-APR-1999; 99US-0129845P.

PR 19-APR-1999; 99US-0130077P.

PR 21-APR-1999; 99US-0130449P.

PR 23-APR-1999; 99US-0130510P.

PR 28-APR-1999; 99US-0130891P.

PR 28-APR-1999; 99US-0131449P.

PR 30-APR-1999; 99US-0132048P.

PR 30-APR-1999; 99US-0132407P.

PR 04-MAY-1999; 99US-0132484P.

PR 05-MAY-1999; 99US-0132485P.

PR 06-MAY-1999; 99US-0132486P.

PR 07-MAY-1999; 99US-0132487P.

PR 11-MAY-1999; 99US-0132863P.

PR 14-MAY-1999; 99US-0134218P.

PR 14-MAY-1999; 99US-0134219P.

PR 14-MAY-1999; 99US-0134221P.

PR 14-MAY-1999; 99US-0134370P.

PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
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PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
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PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
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PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
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PR 21-JUL-1999; 99US-0145086P.
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PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
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PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.

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PR 27-JUL-1999; 99US-0145913P.
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PR 03-AUG-1999; 99US-0147038P.
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PR 08-OCT-1999; 99US-0158232P.
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PR 21-OCT-1999; 99US-0160767P.
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PR 22-OCT-1999; 99US-0160980P.
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PR 22-OCT-1999; 99US-0160989P.
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PR 25-OCT-1999; 99US-0161406P.

PR 26-OCT-1999; 99US-0161359P.
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PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161933P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 9.0%; Score 74; DB 3; Length 769;
Best Local Similarity 100.0%; Pred. No. 2.4e-28;
Matches 74; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 749 GTGGTCTAGAACACTGAAACAGCCGAGCGATCTCTCTCCCTCTCCCTCTCCGATC 808
Db 1 GTGGTCTAGAACACTGAAACAGCCGAGCGATCTCTCTCCCTCTCCCTCTCCGATC 60

Qy 809 CATTCTCCAGCGCA 822
Db 61 CATTCTCCAGCGCA 74

RESULT 4
ADX49209/c
ID ADX49209 standard; cDNA; 485 BP.
XX AC ADX49209;
XX 21-APR-2005 (first entry)
XX Plant full length insert polynucleotide seqid 23949.
KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX Unidentified.
XX US2004034888-A1.
XX 19-FEB-2004.
XX 28-APR-2003; 2003US-00425114.
XX 06-MAY-1999; 99US-00304517.
XX 05-NOV-2001; 2001US-00985678.
(LIUJ/) LIU J.
(ZHOU/) ZHOU Y.
(KOVA/) KOVALIC D K.
(SCRE/) SCREEN S E.
(TABA/) TABASKA J E.
(CAOY/) CAO Y.
XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX New recombinant DNA construct. useful for improving plant tolerance to
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX pests, for conferring increased resistance to plant disease, or for
XX improving yield.
XX Claim 1; SEQ ID NO 23949; 15pp; English.
XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence
XX available in electronic form from the US patent office at
XX ftp.seqdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide
```

CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX SQ Sequence 485 BP; 120 A; 126 C; 129 G; 110 T; 0 U; 0 Other;

Query Match 7.7%; Score 63; DB 13; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.7e-22;
Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 TGCTTGAGATTTTACATCCACCCCTAGACACACTTAGACACAACCTTAAGACAC 242
DB 362 TGCTTGAGATTTTACATCCACCCCTAGACACACTTAGACACAACCTTAAGACAC 303

QY 243 CCA 245
DB 302 CCA 300

RESULT 5
ADX33652
ID ADX33652 standard; cDNA; 821 BP.
XX AC ADX33652;
XX DT 21-APR-2005 (first entry)
XX DE Plant full length insert polynucleotide seqid 16472.
XX KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX OS Unidentified.
XX PN US2004034888-A1.
XX PD 19-FEB-2004.
XX PP 28-APR-2003; 2003US-00425114.
XX PR 06-MAY-1999; 99US-00304517.
XX PR 05-NOV-2001; 2001US-00985678.
XX PA (LIUJ/) LIU J.
XX PA (ZHOU/) ZHOU Y.
XX PA (KOVA/) KOVALIC D K.
XX PA (SCRE/) SCREEN S E.
XX PA (TABA/) TABASKA J E.
XX PA (CAOV/) CAO Y.
XX PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX DR New recombinant DNA construct, useful for improving plant tolerance to
XX PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or

PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX PS Claim 1; SEQ ID NO 16472; 15pp; English.
XX CC The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.sequata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX SQ Sequence 821 BP; 187 A; 227 C; 214 G; 193 T; 0 U; 0 Other;

Query Match 7.5%; Score 62; DB 13; Length 821;
Best Local Similarity 100.0%; Pred. No. 5.7e-22;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 762 CAACTGAAAACAGCCGAGCGATCTCTCTCCCTCTCCCTCTCCGATCCATTCTCCAGCGC 821
DB 1 CAACTGAAAACAGCCGAGCGATCTCTCTCCCTCTCCCTCTCCGATCCATTCTCCAGCGC 60

QY 822 AG 823
DB 61 AG 62

RESULT 6
ADX30094
ID ADX30094 standard; cDNA; 791 BP.
XX AC ADX30094;
XX DT 21-APR-2005 (first entry)
XX DE Plant full length insert polynucleotide seqid 12914.
XX KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX OS Unidentified.
XX PN US2004034888-A1.
XX PD 19-FEB-2004.
XX PP 28-APR-2003; 2003US-00425114.
XX PR 06-MAY-1999; 99US-00304517.
XX PR 05-NOV-2001; 2001US-00985678.
XX PA (LIUJ/) LIU J.
XX PA (ZHOU/) ZHOU Y.
XX PA (KOVA/) KOVALIC D K.
XX PA (SCRE/) SCREEN S E.

XX PF 28-APR-2003; 2003US-00425114.
XX PR 06-MAY-1999; 99US-00304517.
XX PR 05-NOV-2001; 2001US-00985678.
XX (LIUJ/) LIU J.
XX PA (ZHOU/) ZHOU Y.
XX PA (KOVA/) KOVALIC D K.
XX PA (SCRE/) SCREEN S E.
XX PA (TABAS/) TABASKA J E.
XX PA (CAOY/) CAO Y.
XX PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX WPI; 2004-180133/17.
XX New recombinant DNA construct, useful for improving plant tolerance to
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
PT pests, for conferring increased resistance to plant disease, or for
PT improving yield.
XX Claim 1; SEQ ID NO 16676; 15pp; English.
XX The invention describes a recombinant DNA construct comprising a
CC polynucleotide consisting of a sequence encoding an amino acid sequence
CC available in electronic form from the US patent office at
CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
CC of the invention are also useful in physical arrays of molecules and as
CC plant breeding markers. The recombinant DNA construct is useful for
CC improving plant tolerance to cold, heat, drought, herbicides, extreme
CC osmotic conditions, pathogens or pests, for manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, for conferring
CC increased resistance to plant disease, for producing galactomannan,
CC lignin or plant growth regulators, for increasing the rate of homologous
CC recombination in plants, for improving yield by modification of
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC or by providing improved plant growth and development under at least one
CC stress condition or for modifying seed oil or protein yield and/or
CC content. This sequence represents a plant full length insert
CC polynucleotide that can be used in the recombinant DNA construct of the
CC invention.
XX SQ Sequence 781 BP; 175 A; 216 C; 209 G; 181 T; 0 U; 0 Other;
Query Match 6.0%; Score 49; DB 13; Length 781;
Best Local Similarity 100.0%; Pred. No. 4.5e-15;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 775 CCGAGCGATCTCCCTCTCCCTCTCCCTCTCCGATCCATTCCTCCAGCGCAG 823
DB 1 CCGAGCGATCTCCCTCTCCCTCTCCCTCTCCGATCCATTCCTCCAGCGCAG 49
RESULT 9
ABL76691
ID ABL76691 standard; cDNA; 307 BP.
XX ABL76691;
XX 14-MAY-2002 (first entry)
XX Corn tassal-derived polynucleotide (cdps) SEQ ID NO:6065.
XX Corn; corn tassal-derived polynucleotide; cdps; hybrid breeding; CDPS;
KW inheritance; characteristic; growth; development; disease resistance;
KW environmental adaptability; quality; yield; molecular marker;
KW multigene trait; plant breeding; corn tassal; gene; ss.
XX Zea mays.
OS US2001051335-A1.
XX PN

PD 13-DEC-2001.
XX 16-APR-1999; 99US-00294093.
XX 21-APR-1998; 98US-0082567P.
XX (LALG/) LALGUDI R V.
XX PA (ITOL/) ITO L Y.
XX PA (SHER/) SHERMAN B K.
XX PI Lalgudi RV, Ito LY, Sherman BK;
XX WPI; 2002-163647/21.
XX Novel purified corn tassal-derived polynucleotide useful for determining
PT altered gene expression, to recover regulatory elements and to follow
PT inheritance of desirable characteristics through hybrid breeding
PT programs.
XX Claim 1; SEQ ID NO 6065; 201pp; English.
XX The present sequence describes a purified corn tassal-derived
CC polynucleotide sequence (cdps) comprising a nucleic acid sequence
CC selected from those given in ABL70627 to ABL76833. The cdps sequences
CC encode corn tassal-derived polypeptides (CDPS). The cdps sequences (I)
CC can be used for determining altered gene expression, to recover
CC regulatory elements and to follow inheritance of desirable
CC characteristics through hybrid breeding programs. (I) are also useful in
CC the evaluation, and alteration of desired characteristics associated with
CC growth and development, disease resistance, environmental adaptability,
CC quality and yield, and as molecular markers for studying inheritance of
CC multigene traits in a plant breeding program. (I) can be used to produce
CC a tassal-specific profile of gene transcription, a transcript image, to
CC clone regulatory elements for use in transformation vectors, to express a
CC polypeptide, to identify, isolate or extend identical or related corn
CC tassal nucleic acid sequences from DNA libraries, in nucleic acid
CC hybridisation or amplification technologies, as query sequences to
CC determine homology of known sequences, as probe for use in Southern or
CC Northern hybridisation, and to identify the presence of and/or to
CC determine the degree of similarity between two (or more) nucleic acid
CC sequences
XX SQ Sequence 307 BP; 63 A; 99 C; 81 G; 50 T; 0 U; 14 Other;
Query Match 4.9%; Score 40; DB 6; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 784 CTCCTCTCCCTCTCCCTCTCCGATCCATTCCTCCAGCGCAG 823
DB 1 CTCCTCTCCCTCTCCCTCTCCGATCCATTCCTCCAGCGCAG 40
RESULT 10
ADX60974
ID ADX60974 standard; cDNA; 1326 BP.
XX AC ADX60974;
XX 21-APR-2005 (first entry)
XX Plant full length insert polynucleotide seqid 31817.
XX plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX Unidentified.
OS

XX PN US2004034888-A1.
 XX PD 19-FEB-2004.
 XX PF 28-APR-2003; 2003US-00425114.
 XX PR 06-MAY-1999; 99US-00304517.
 XX PR 05-NOV-2001; 2001US-00985678.
 XX XX (LIUJ/) LIU J.
 XX XX (ZHOU/) ZHOU Y.
 XX PA (KOVA/) KOVALIC D K.
 XX PA (SCRE/) SCREEN S E.
 XX PA (TABAS/) TABASKA J E.
 XX PA (CAOY/) CAO Y.
 XX XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX WPI; 2004-180133/17.
 XX New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX Claim 1; SEQ ID NO 31817; 15pp; English.
 XX The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This sequence represents a plant full length insert
 CC polynucleotide that can be used in the recombinant DNA construct of the
 XX invention.
 XX Sequence 1326 BP; 353 A; 297 C; 299 G; 377 T; 0 U; 0 Other;
 SQ Query Match 4.9%; Score 40; DB 13; Length 1326;
 Best Local Similarity 100.0%; Pred. No. 2.7e-10;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 48 CAGTGTCTATCTTAAACATGCTGTCTTACCATATTCATT 87
 DB 181 CAGTGTCTATCTTAAACATGCTGTCTTACCATATTCATT 220
 RESULT 11
 ADX33827
 ID ADX33827 standard; cDNA; 782 BP.
 XX AC ADX33827;
 XX DT 21-APR-2005 (first entry)
 XX DE Plant full length insert polynucleotide seqid 16647.
 XX KW plant protectant; plant growth regulator; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;

KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 XX protein content; gene; ss.
 OS Unidentified.
 XX US2004034888-A1.
 XX PN 19-FEB-2004.
 XX PD 28-APR-2003; 2003US-00425114.
 XX PF 06-MAY-1999; 99US-00304517.
 XX PR 05-NOV-2001; 2001US-00985678.
 XX XX (LIUJ/) LIU J.
 XX XX (ZHOU/) ZHOU Y.
 XX PA (KOVA/) KOVALIC D K.
 XX PA (SCRE/) SCREEN S E.
 XX PA (TABAS/) TABASKA J E.
 XX PA (CAOY/) CAO Y.
 XX XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 XX WPI; 2004-180133/17.
 XX New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 XX Claim 1; SEQ ID NO 16647; 15pp; English.
 XX The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This sequence represents a plant full length insert
 CC polynucleotide that can be used in the recombinant DNA construct of the
 XX invention.
 XX Sequence 782 BP; 177 A; 214 C; 207 G; 184 T; 0 U; 0 Other;
 SQ Query Match 4.4%; Score 36; DB 13; Length 782;
 Best Local Similarity 100.0%; Pred. No. 3.5e-08;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 788 TCTCCCTCTCCCTCTCCGATCCATTCCTCCAGCGCAG 823
 DB 1 TCTCCCTCTCCCTCTCCGATCCATTCCTCCAGCGCAG 36
 RESULT 12
 ADX48086/c
 ID ADX48086 standard; cDNA; 1578 BP.
 XX AC ADX48086;
 XX DT 21-APR-2005 (first entry)
 XX DE Plant full length insert polynucleotide seqid 22826.
 XX KW

KW plant protectant; plant growth regulant; gene therapy; plant;
KW recombinant DNA construct; physical array; plant breeding marker;
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
KW extreme osmotic condition; pathogen tolerance; pest tolerance;
KW growth rate; cell cycle pathway; disease resistance;
KW galactomannan production; lignin production; plant growth regulator;
KW yield; plant growth; plant development; seed oil; protein yield;
KW protein content; gene; ss.
XX Unidentified.
OS
XX
XX
PN US2004034888-A1.
XX
PD
XX
XX 19-FEB-2004.
XX
PF 28-APR-2003; 2003US-00425114.
XX
XX
PR 06-MAY-1999; 99US-00304517.
PR 05-NOV-2001; 2001US-00985678.
XX
XX
PA (LIUJ/) LIU J.
PA (ZHOU/) ZHOU Y.
PA (KOVA/) KOVALIC D K.
PA (SCRE/) SCREEN S E.
PA (TABA/) TABASKA J E.
PA (CAOY/) CAO Y.
XX
XX
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
XX
XX WPI; 2004-180133/17.
XX
XX New recombinant DNA construct, useful for improving plant tolerance to
XX cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
XX pests, for conferring increased resistance to plant disease, or for
XX improving yield.
XX
XX
PS Claim 1; SEQ ID NO 22826; 15pp; English.
XX
XX The invention describes a recombinant DNA construct comprising a
XX polynucleotide consisting of a sequence encoding an amino acid sequence
XX available in electronic form from the US patent office at
XX ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
XX of the invention are also useful in physical arrays of molecules and as
XX plant breeding markers. The recombinant DNA construct is useful for
XX improving plant tolerance to cold, heat, drought, herbicides, extreme
XX osmotic conditions, pathogens or pests, for manipulating growth rate in
XX plant cells by modification of the cell cycle pathway, for conferring
XX increased resistance to plant disease, for producing galactomannan,
XX lignin or plant growth regulators, for increasing the rate of homologous
XX recombination in plants, for improving yield by modification of
XX photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
XX or by providing improved plant growth and development under at least one
XX stress condition or for modifying seed oil or protein yield and/or
XX content. This sequence represents a plant full length insert
XX polynucleotide that can be used in the recombinant DNA construct of the
XX invention.
XX
SQ Sequence 1578 BP; 380 A; 391 C; 429 G; 378 T; 0 U; 0 Other;
Query Match 4.4%; Score 36; DB 13; Length 1578;
Best Local Similarity 100.0%; Pred. No. 3.6e-08;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 148 ATAGAGCTAAGACACTGTGCTTCGTCAGATACAT 183
DB 908 ATAGAGCTAAGACACTGTGCTTCGTCAGATACAT 873
RESULT 13
AA57891
ID AAA57891 standard; DNA; 6343 BP.
XX
XX
XX AAA57891;

XX 10-OCT-2000 (first entry)
DT
XX
XX Maize glossy2 (gl2) gene.
DE
XX
XX Maize; glossy2; gl2; cuticle; cuticular lipid biosynthesis;
KW lipid composition; lipid quantity; disease resistance; pest resistance;
KW wind resistance; frost resistance; UV resistance; transgenic plant;
KW antisense inhibition; ds.
XX
OS
XX Zea mays.
XX
XX US6060644-A.
XX
XX
XX 09-MAY-2000.
XX
XX
XX 29-DEC-1995; 95US-00581148.
XX
XX 24-MAR-1994; 94US-00218028.
XX
XX (IOWA) UNIV IOWA STATE RES FOUND INC.
XX
XX Schnable PS, Nikolau BJ, Xu X, Xia Y, Robertson DS, Hansen JD;
PI
XX
XX WPI; 2000-349707/30.
XX
XX
XX Transforming plants such as maize and canola, for producing new plant
XX varieties having disease and pest resistance involves introducing
XX cuticular lipid genes into the plant genome.
XX
XX Example 7; Col 115-122; 69pp; English.
XX
XX The invention relates to transforming a plant cell with either a nucleic
XX acid encoding a plant cuticular lipid biosynthetic protein, or an
XX antisense nucleic acid sequence targeted to a plant cuticular lipid
XX gene, and then generating a plant from the plant cell. The cuticular
XX lipid genes that may be used in the invention are given in AAA57891-
XX A57884 and AAA57891. The cuticle consists of a meshwork (cutin) of cross-
XX esterified polymerised hydroxy-fatty acids embedded in a complex mixture
XX of nonpolar lipids (the cuticular wax). The cuticle protects and
XX strengthens the plants, prevents evaporation of internal fluids and
XX filters UV radiation. Mutations in the cuticular lipid genes affects the
XX quantity and composition of cuticular lipids; in maize, 17 loci (the
XX glossy (gl) genes) have been identified as being involved in cuticular
XX lipid biosynthesis or control. The method is useful for introducing a
XX nucleic acid into a cell preferably of maize, soybean, rapeseed, canola,
XX cotton, safflower, peanut, palm or sunflower plant and generating a plant
XX from the plant cell. The transformed plants have improved environmental
XX resistance relating to wind, frost, UV or drought; fungal, bacterial or
XX viral disease resistance; pest resistance; and altered lipid content in
XX seeds. The present sequence represents the maize glossy2 (gl2) gene
XX
SQ Sequence 6343 BP; 1493 A; 1667 C; 1607 G; 1564 T; 0 U; 12 Other;
Query Match 4.4%; Score 36; DB 3; Length 6343;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 101 CATTCAATAAATTAAGTGACCAATCAGATAGTCTC 136
DB 3715 CATTCAATAAATTAAGTGACCAATCAGATAGTCTC 3750
RESULT 14
AAV63717
ID AAV63717 standard; DNA; 6550 BP.
XX
XX
XX AAV63717;
XX
XX
XX 12-APR-1999 (first entry)
DT
XX
XX Maize per5 root preferential cationic peroxidase gene.
XX
XX

```
KW Peroxidase; per5 gene; maize; corn; transgenic plant; promoter; root; ds.
XX Zea mays.
OS
XX
XX
XX Key
XX promoter
XX
XX Location/Qualifiers
XX 1..4215
XX /tag= a
XX /note= "this region is specifically claimed in Claim 1"
XX 1..4200
XX /tag= c
XX /note= "this region is specifically claimed in Claim 1"
XX 1..4148
XX /tag= b
XX /note= "this region is specifically claimed in Claim 1"
XX 2532..4215
XX /tag= f
XX /note= "this region is specifically claimed in Claim 1"
XX 2532..4200
XX /tag= e
XX /note= "this region is specifically claimed in Claim 1"
XX 2532..4148
XX /tag= d
XX /note= "this region is specifically claimed in Claim 1"
XX 3187..4215
XX /tag= i
XX /note= "this region is specifically claimed in Claim 1"
XX 3187..4200
XX /tag= h
XX /note= "this region is specifically claimed in Claim 1"
XX 3187..4148
XX /tag= g
XX /note= "this region is specifically claimed in Claim 1"
XX 4086..4215
XX /tag= l
XX /note= "this region is specifically claimed in Claim 1"
XX 4086..4200
XX /tag= k
XX /note= "this region is specifically claimed in Claim 1"
XX 4086..4148
XX /tag= j
XX /note= "this region is specifically claimed in Claim 1"
XX 4201..6068
XX /tag= m
XX /product= "peroxidase"
XX /note= "contains introns"
XX 4201..4425
XX /tag= n
XX /number= 1
XX 4420..5064
XX /tag= o
XX /note= "this sequence is specifically claimed in Claim 2"
XX 4426..5058
XX /tag= p
XX /number= 1
XX /note= "this intron is specifically claimed in Claim 2"
XX 5059..5250
XX /tag= q
XX /number= 2
XX 5245..5388
XX /tag= r
XX /note= "this sequence is specifically claimed in Claim 2"
XX 5251..5382
XX /tag= s
XX /number= 2
XX /note= "this intron is specifically claimed in Claim 2"
XX 5383..5548
XX /tag= t
XX /number= 3
XX 5542..5654
XX /tag= u
XX /note= "this sequence is specifically claimed in Claim 2"
XX 5542..5654
XX /tag= x
```

```
FT intron
FT 5549..5649
FT /tag= v
FT /number= 3
FT /note= "this intron is specifically claimed in Claim 2"
FT 5650..6065
FT /tag= w
FT /number= 4
FT 6068..6431
FT /tag= y
FT /note= "transcription termination sequence, specifically
FT claimed in Claim 3"
XX
XX WO9856921-A1.
XX
XX 17-DEC-1998.
XX
XX 10-JUN-1998; 98WO-US011921.
XX
XX 12-JUN-1997; 97US-0049752P.
XX
XX (DOWC ) DOW AGROSCIENCES LLC.
XX
XX Ainley M, Armstrong K, Belmar S, Folkerts O, Hopkins N, Menke MA;
XX Paredy D, Petolino JF, Smith K, Woosley A;
XX
XX WPI; 1999-080904/07.
XX P-PSDB; AAW87893.
XX
XX New isolated regulatory sequences for transgenic plants - which are
XX derived from the maize root preferential cationic peroxidase protein
XX (per5) gene.
XX
XX Claim 1; Page 84-89; 150pp; English.
XX
XX This is the nucleotide sequence of the maize per5 root preferential
XX cationic peroxidase gene, which encodes a 333-amino acid peroxidase
XX polypeptide (see AAW87893). Genomic clones comprising per5 sequences were
XX isolated from a maize W22 genomic library using a probe based on isolated
XX per5 cDNA. Overlapping subfragments of the gene were sequenced to
XX determine the complete 6550 bp sequence of the per5 gene. Regulatory
XX sequences derived from the per5 gene, including the promoter, introns and
XX 3' untranslated region (3'UTR), are used in claimed recombinant gene
XX cassettes for controlling expression of recombinant genes in selected
XX tissue, especially the root, of transformed plants, particularly maize.
XX The gene cassettes can be used for expression of heterologous genes such
XX as those that confer tolerance to herbicides, insects or viruses, and
XX genes that provide improved nutritional value or processing
XX characteristics to the plant. Use of the per5 3'UTR sequences provides
XX enhanced expression compared to similar gene cassettes utilizing the nos
XX 3'UTR
XX
XX Query Match 3.9%; Score 32; DB 2; Length 6550;
XX Best Local Similarity 100.0%; Pred. No. 4.9e-06;
XX Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 59 TCTAAACATGTGTTTACCATTATTCATTGTA 90
XX |||||
XX Db 1415 TCTAAACATGTGTTTACCATTATTCATTGTA 1446
XX
XX
XX RESULT 15
XX AAV63730
XX ID AAV63730 standard; DNA; 9299 BP.
XX
XX AC AAV63730;
XX
XX 12-APR-1999 (first entry)
XX
XX DE Vector plasmid PerGUS16.
```

KW Peroxidase; per5 gene; maize; corn; transgenic plant; promoter; root;
KW vector; plasmid perGUS16; beta-glucuronidase; uidA; reporter gene; ds;
KW circular; cyclic.
XX
OS Escherichia coli.
OS Zea mays.
OS Agrobacterium tumefaciens.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT promoter 48..4247
FT /tag= a
FT /note= "per5 promoter and untranslated leader"
FT exon 4248..4263
FT /tag= b
FT /note= "per5 exon 1"
FT CDS 4264..6068
FT /tag= c
FT /product= "beta-glucuronidase"
FT /note= "Escherichia coli uidA reporter gene"
FT 3'UTR 6069..6111
FT /tag= d
FT /note= "3' untranslated region from pBI221"
FT 3'UTR 6122..6396
FT /tag= e
FT /note= "nos 3'UTR"
FT misc_feature 6397..6407
FT /tag= f
FT /note= "linker"
FT misc_feature 6408..9299
FT /tag= g
FT /note= "Bluescript II SK-"
XX
FN WO9856921-A1.
XX
XX 17-DEC-1998.
XX
XX 10-JUN-1998; 98WO-US011921.
XX
XX 12-JUN-1997; 97US-0049752P.
XX
XX (DOWC) DOW AGROSCIENCES LLC.
XX
XX Ainley M, Armstrong K, Belmar S, Folkerts O, Hopkins N, Menke MA,
XX Pareddy D, Petolino JF, Smith K, Woosley A;
XX WPI; 1999-080904/07.
XX
XX New isolated regulatory sequences for transgenic plants - which are
XX derived from the maize root preferential cationic peroxidase protein
XX (per5) gene.
XX
XX Example 11; Page 108-112; 150pp; English.
XX
XX This is the nucleotide sequence of PerGUS, a plasmid containing 4 kb of
XX the maize root preferential cationic peroxidase per5 gene comprising the
XX per5 promoter, untranslated leader, and the first 5 codons of the coding
XX region (i.e. nucleotides 1-4200 of the sequence given in AAV63717), as
XX well as the GUS gene, and the nos 3' untranslated region (3'UTR). It does
XX not include an intron in the untranslated region. The invention relates
XX to new isolated regulatory sequences, especially promoter, intron and
XX 3'UTR sequences, of the maize per5 gene. Claimed recombinant gene
XX cassettes comprising per5 regulatory sequences are used to control
XX expression of recombinant genes in selected tissue, especially the root,
XX of transformed plants, particularly maize
XX
SQ Sequence 9299 BP; 2573 A; 2114 C; 2158 G; 2453 T; 0 U; 1 Other;
Query Match 3.9%; Score 32; DB 2; Length 9299;
Best Local Similarity 100.0%; Pred. No. 4.9e-06;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 TCTAATAACATGTGCTTACCATATTCATTGTA 90
DB 1462 TCTAATAACATGTGCTTACCATATTCATTGTA 1493

Search completed: March 5, 2006, 11:35:52
Job time : 560 secs

```
DRIGIN
Query Match 4.5%; Score 37; DB 14; Length 198102;
Best Local Similarity 100.0%; Pred. No. 4.9e-10; Indels 0; Gaps 0;
Matches 37; Conservative 0; Mismatches 0;

Qy 92 CAATCAGAACATTCATTAATTAAGTGACCAATCAG 128
Db 173568 CAATCAGAACATTCATTAATTAAGTGACCAATCAG 173604

/estimated_length=100

RESULT 13
ZMGLOSSY
LOCUS ZMGLOSSY 6343 bp DNA linear PLN 09-MAY-1996
DEFINITION Z.mays Glossy2 locus DNA.
ACCESSION X88779
VERSION X88779.1 GI:949979
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1
AUTHORS Tacke, E., Korfhage, C., Michel, D., Maddaloni, M., Motto, M.,
Lanzini, S., Salamini, F. and Döring, H.P.
TITLE Transposon tagging of the maize Glossy2 locus with the transposable
element En/Spm
JOURNAL Plant J. 8 (6), 907-917 (1995).
PUBMED 8580961
REFERENCE 2 (bases 1 to 6343)
AUTHORS Tacke, E.
TITLE Direct Submission
JOURNAL Submitted (19-JUN-1995) E. Tacke, Max-Planck-Institute, Dept.
Salamini, Carl-von-Linne-Weg 10, 50829 Köln, NRW, FRG
FEATURES
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LAIGFVAHLIGDIPSAATCFNKWAQILSGKKEATVLTTPNQPLOSQSPAAPRSVKQ
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/number=1
3924..5001
/number=2

mRNA
exon
gene
CDS
intron
exon

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.6e-09;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 CATTCAATAAATTAAGTGACCAATCAGATAGTCTC 136
Db 3715 CATTCAATAAATTAAGTGACCAATCAGATAGTCTC 3750

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DEFINITION Zea mays clone ZMBBB0309E13, *** SEQUENCING IN PROGRESS ***, 7
unordered pieces.
ACCESSION AC149816
VERSION AC149816.2 GI:57790137
KEYWORDS HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEPIN.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 69497)
AUTHORS Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bhatti, A.K.
and Messing, J.
TITLE Zea mays, clone ZMBBB0309E13
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 69497)
AUTHORS Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bhatti, A.K.,
Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S.,
Archachi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L.,
Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J.S., Dodge, S.,
Dooley, K., Dorris, L., Erickson, J., Fero, S., Ferreira, P.,
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Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
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Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C.,
Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,
Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
TITLE Direct Submission
JOURNAL Submitted (22-JUN-2004) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
REFERENCE 3 (bases 1 to 69497)
AUTHORS Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bhatti, A.K.,
Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S.,
Archachi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L.,
Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J.S., Dodge, S.,
Dooley, K., Dorris, L., Erickson, J., Fero, S., Ferreira, P.,
FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L.,
Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J.,
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P.,
Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J.,
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Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C.,
Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,
Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
TITLE Direct Submission
JOURNAL Submitted (03-FEB-2005) Broad Institute of MIT and Harvard, 320
Charles Street, Cambridge, MA 02141, USA
```

KW plant protectant; plant growth regulant; gene therapy; plant;
 KW recombinant DNA construct; physical array; plant breeding marker;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
 KW extreme osmotic condition; pathogen tolerance; pest tolerance;
 KW growth rate; cell cycle pathway; disease resistance;
 KW galactomannan production; lignin production; plant growth regulator;
 KW yield; plant growth; plant development; seed oil; protein yield;
 KW protein content; gene; ss.
 XX Unidentified.
 OS
 XX
 XX US2004034888-A1.
 PN
 XX
 PD 19-FEB-2004.
 XX
 XX
 PF 28-APR-2003; 2003US-00425114.
 XX
 XX 06-MAY-1999; 99US-00304517.
 PR
 PR 05-NOV-2001; 2001US-00985678.
 XX
 XX (LIU//) LIU J.
 PA (ZHOU//) ZHOU Y.
 PA (KOVA//) KOVALIC D K.
 PA (SCRE//) SCREEN S E.
 PA (TAB//) TABASKA J E.
 PA (CAOY//) CAO Y.
 XX
 XX
 XX Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;
 PI
 XX
 XX WPI; 2004-180133/17.
 DR
 XX
 XX New recombinant DNA construct, useful for improving plant tolerance to
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or
 PT pests, for conferring increased resistance to plant disease, or for
 PT improving yield.
 PS
 PS Claim 1; SEQ ID NO 22826; 15pp; English.
 XX
 CC The invention describes a recombinant DNA construct comprising a
 CC polynucleotide consisting of a sequence encoding an amino acid sequence
 CC available in electronic form from the US patent office at
 CC ftp.segdata.uspto.gov/sequence.html?DocID:2004034888. The polynucleotide
 CC of the invention are also useful in physical arrays of molecules and as
 CC plant breeding markers. The recombinant DNA construct is useful for
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in
 CC plant cells by modification of the cell cycle pathway, for conferring
 CC increased resistance to plant disease, for producing galactomannan,
 CC lignin or plant growth regulators, for increasing the rate of homologous
 CC recombination in plants, for improving yield by modification of
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
 CC or by providing improved plant growth and development under at least one
 CC stress condition or for modifying seed oil or protein yield and/or
 CC content. This sequence represents a plant full length insert
 CC polynucleotide that can be used in the recombinant DNA construct of the
 CC invention.
 XX
 SQ Sequence 1578 BP; 380 A; 391 C; 429 G; 378 T; 0 U; 0 Other;
 Query Match 4.4%; Score 36; DB 13; Length 1578;
 Best Local Similarity 100.0%; Pred. No. 3.6e-08;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 148 ATAGAGCTAAGACACTGTCTTCTTCGTCAAGATACAT 183
 DB 908 ATAGAGCTAAGACACTGTCTTCTTCGTCAAGATACAT 873
 RESULT 13
 AAAS7891
 ID AAAS7891 standard; DNA; 6343 BP.
 XX
 AC AAAS7891;

XX 10-OCT-2000 (first entry)
 DT
 XX
 DE Maize glossy2 (gl2) gene.
 XX
 KW Maize; glossy2; gl2; cuticle; cuticular lipid biosynthesis;
 KW lipid composition; lipid quantity; disease resistance; pest resistance;
 KW wind resistance; frost resistance; UV resistance; transgenic plant;
 KW antisense inhibition; db.
 XX
 OS
 XX Zea mays.
 PN
 XX US6060644-A.
 PD
 XX 09-MAY-2000.
 XX
 PF 29-DEC-1995; 95US-00581148.
 PR
 PR 24-MAR-1994; 94US-00218028.
 XX
 PA (IOWA) UNIV IOWA STATE RES FOUND INC.
 XX
 XX Schnable PS, Nikolau BJ, Xu X, Xia Y, Robertson DS, Hansen JD;
 PI
 XX WPI; 2000-349707/30.
 DR
 XX
 XX Transforming plants such as maize and canola, for producing new plant
 PT varieties having disease and pest resistance involves introducing
 PT cuticular lipid genes into the plant genome.
 XX
 PS Example 7; Col 115-122; 69pp; English.
 XX
 CC The invention relates to transforming a plant cell with either a nucleic
 CC acid encoding a plant cuticular lipid biosynthetic protein, or an
 CC antisense nucleic acid sequence targeted to a plant cuticular lipid
 CC gene, and then generating a plant from the plant cell. The cuticular
 CC lipid genes that may be used in the invention are given in AAAS7871-
 CC A57884 and AAAS7891. The cuticle consists of a meshwork (cutin) of cross-
 CC esterified polymerised hydroxy-fatty acids embedded in a complex mixture
 CC of nonpolar lipids (the cuticular wax). The cuticle protects and
 CC strengthens the plants, prevents evaporation of internal fluids and
 CC filters UV radiation. Mutations in the cuticular lipid genes affects the
 CC quantity and composition of cuticular lipids; in maize, 17 loci (the
 CC glossy (gl) genes) have been identified as being involved in cuticular
 CC lipid biosynthesis or control. The method is useful for introducing a
 CC nucleic acid into a cell preferably of maize, soybean, rapeseed, canola,
 CC cotton, safflower, peanut, palm or sunflower plant and generating a plant
 CC from the plant cell. The transformed plants have improved environmental
 CC resistance relating to wind, frost, UV or drought; fungal, bacterial or
 CC viral disease resistance; pest resistance; and altered lipid content in
 CC seeds. The present sequence represents the maize glossy2 (gl2) gene
 XX
 SQ Sequence 6343 BP; 1493 A; 1667 C; 1607 G; 1564 T; 0 U; 12 Other;
 Query Match 4.4%; Score 36; DB 3; Length 6343;
 Best Local Similarity 100.0%; Pred. No. 3.7e-08;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 101 CATTCAATAAATTAAAGTGACCAATCAGATAGTCTC 136
 DB 3715 CATTCAATAAATTAAAGTGACCAATCAGATAGTCTC 3750
 RESULT 14
 AAAS7891
 ID AAAS7891 standard; DNA; 6550 BP.
 XX
 AC AAAS7891;
 XX
 XX 12-APR-1999 (first entry)
 DT
 XX Maize per5 root preferential cationic peroxidase gene.
 DE
 XX

KW Peroxidase; per5 gene; maize; corn; transgenic plant; promoter; root; ds.
 XX Zea mays.
 OS
 FH Key Location/Qualifiers
 FT promoter 1. .4215
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 FT /note= "this region is specifically claimed in Claim 1"
 FT 1. .4200
 FT /tag= c
 FT /note= "this region is specifically claimed in Claim 1"
 FT 1. .4148
 FT /tag= b
 FT /note= "this region is specifically claimed in Claim 1"
 FT 2532. .4215
 FT /tag= f
 FT /note= "this region is specifically claimed in Claim 1"
 FT 2532. .4200
 FT /tag= e
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 FT /note= "contains introns"
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 FT /tag= x

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 FT /number= 3
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 FT /tag= w
 FT /number= 4
 FT 6068. .6431
 FT /tag= y
 FT /note= "transcription termination sequence, specifically
 FT claimed in Claim 3"
 XX
 PN WO9856921-A1.
 XX 17-DEC-1998.
 PD
 PF 10-JUN-1998; 98WO-US011921.
 XX
 PR 12-JUN-1997; 97US-0049752P.
 XX
 PA (DOWC) DOW AGROSCIENCES LLC.
 XX
 PI Ainley M, Armstrong K, Belmar S, Folkerts O, Hopkins N, Menke MA;
 PI Pareddy D, Petolino JF, Smith K, Woosley A;
 XX
 DR WPI; 1999-080904/07.
 DR P-PSDB; RAN87893.
 XX
 XX New isolated regulatory sequences for transgenic plants - which are
 FT derived from the maize root preferential cationic peroxidase protein
 FT (per5) gene.
 XX
 PS Claim 1; Page 84-89; 150pp; English.
 CC This is the nucleotide sequence of the maize per5 root preferential
 CC cationic peroxidase gene, which encodes a 333-amino acid peroxidase
 CC polypeptide (see RAN87893). Genomic clones comprising per5 sequences were
 CC isolated from a maize W22 genomic library using a probe based on isolated
 CC per5 cDNA. Overlapping subfragments of the gene were sequenced to
 CC determine the complete 6550 bp sequence of the per5 gene. Regulatory
 CC sequences derived from the per5 gene, including the promoter, introns and
 CC 3' untranslated region (3'UTR), are used in claimed recombinant gene
 CC cassettes for controlling expression of recombinant genes in selected
 CC tissue, especially the root, of transformed plants, particularly maize.
 CC The gene cassettes can be used for expression of heterologous genes such
 CC as those that confer tolerance to herbicides, insects or viruses, and
 CC genes that provide improved nutritional value or processing
 CC characteristics to the plant. Use of the per5 3'UTR sequences provides
 CC enhanced expression compared to similar gene cassettes utilising the nos
 CC 3'UTR
 XX
 SQ Sequence 6550 BP; 1844 A; 1427 C; 1346 G; 1933 T; 0 U; 0 Other;
 Query Match 3.9%; Score 32; DB 2; Length 6550;
 Best Local Similarity 100.0%; Pred.No. 4.9e-06;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 59 TCTAAACATGCTCTTACCATTTCATTGTA 90
 DB 1415 TCTAAACATGCTCTTACCATTTCATTGTA 1446
 RESULT 15
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 ID AAV63730 standard; DNA; 9299 BP.
 XX
 AC AAV63730;
 XX
 DT 12-APR-1999 (first entry)
 XX
 DE Vector plasmid perGUS16.
 XX

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Db	241	ACCCATTGTACATGCCCTAACTGGCACCGCTACGTAGGGGCTATTCAAGAACCAACCATG	300		
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Db	301	TACAGTTGTTGCAACGTAATGGTTATTGCTTCAGATTAAGCTAAATTTATAGACTGA	360		
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Db	361	TGCAGCTGCAATTCATAGACACAAAACAGTGTAGAGCCGTATAGCAATTAAGCAACA	420		
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Qy	601	TTCTGTTTCTAGTCAACATCGCTCGATCCACGGGGAGCGAGGACGAATGTGTGGCCC	660		
Db	601	TTCTGTTTCTAGTCAACATCGCTCGATCCACGGGGAGCGAGGACGAATGTGTGGCCC	660		
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Qy	721	ATATACAGACGACGATACCCATATCGTGTGTAGAGCAACTGAAACAGCCGAGC	780		
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RESULT 2	AX299946	1587 bp	DNA	linear	PAT 26-NOV-2001
LOCUS	Sequence 87 from Patent WO0183790.				
DEFINITION	AX299946				
ACCESSION	AX299946				
VERSION	AX299946.1	GI:17129437			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					
ORIGIN					
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Best Local Similarity	100.0%;	Pred. No. 4e-278;			
Matches 473;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
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Center name: TIGR
Seq_lib_id: ZOCR

Web site: <http://www.tigr.org/tdb/tgi/maize/>
Contact: maize@tigr.org

* NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 2769: contig of 2769 bp in length
* 2770 2869: gap of unknown length
* 2870 23820: contig of 20951 bp in length
* 23821 23920: gap of unknown length
* 23921 68663: contig of 44743 bp in length
* 68664 68763: gap of unknown length
* 68764 103952: contig of 33189 bp in length
* 103953 102052: gap of unknown length
* 102053 105474: contig of 3422 bp in length
* 105475 105574: gap of unknown length
* 105575 110248: contig of 4674 bp in length
* 110249 110348: gap of unknown length
* 110349 112741: contig of 2393 bp in length
* 112742 112841: gap of unknown length
* 112842 120977: contig of 8136 bp in length
* 120978 121078: gap of unknown length
* 121079 125183: contig of 4106 bp in length
* 125184 125283: gap of unknown length
* 125284 127032: contig of 1748 bp in length
* 127033 127131: gap of unknown length
* 127132 143472: contig of 16341 bp in length
* 143473 143572: gap of unknown length
* 143573 147242: contig of 3670 bp in length
* 147243 147343: gap of unknown length
* 147343 149882: contig of 2540 bp in length.

FEATURES

source

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ORIGIN

Query Match

12.5% Score 103; DB 14; Length 149882;

Best Local Similarity 100.0%; Pred. No. 1.3e-50;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 143 CGAATATAGAGCTAAGACACTGTGTCTTCGTCAGATACATGTCTTGAGATTTTACAT 202
Db 51039 CGAATATAGAGCTAAGACACTGTGTCTTCGTCAGATACATGTCTTGAGATTTTACAT 50980
Qy 203 TCACCCCTAGACACACTCTAGACACAACTTAAGACACCA 245
Db 50979 TCACCCCTAGACACACTCTAGACACAACTTAAGACACCA 50937

RESULT 4

AC155608 LOCUS 182004 bp DNA linear HTG 25-JAN-2005
DEFINITION Zea mays strain B73 clone ZMMBB0261N01, *** SEQUENCING IN PROGRESS
***, 31 unordered pieces.

ACCESSION AC155608

VERSION AC155608.2 GI:58082467

KEYWORDS HTG; HTGS_PHASE1.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

AUTHORS

Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
Quackenbush, J.
Consortium for Maize Genomics - BAC skim sequencing and assembly
Unpublished

TITLE

JOURNAL

REFERENCE

AUTHORS

Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
Quackenbush, J.

TITLE

JOURNAL

REFERENCE

AUTHORS

Submitted (15-JAN-2005) The Institute for Genomic Research (TIGR),
9712 Medical Center Dr, Rockville, MD 20850

TITLE

JOURNAL

REFERENCE

AUTHORS

Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlfing, T.,
Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
Quackenbush, J.

TITLE

JOURNAL

COMMENT

Submitted (25-JAN-2005) The Institute for Genomic Research (TIGR),
9712 Medical Center Dr, Rockville, MD 20850

On Jan 25, 2005 this sequence version replaced gi:57863129.

----- Trace submission

Center name: TIGR

Seq_lib_id: ZGGF

----- Project information

Web site: <http://www.tigr.org/tdb/tgi/maize/>

Contact: maize@tigr.org

* NOTE: This is a 'working draft' sequence. It currently
* consists of 31 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 2004: contig of 2004 bp in length
* 2005 2104: gap of unknown length
* 2105 15140: contig of 13036 bp in length
* 15141 15240: gap of unknown length
* 15241 16541: contig of 1301 bp in length
* 16542 16641: gap of unknown length

* 16642	21576:	contig of 4935 bp in length	gap	/estimated_length=unknown
* 21577	21676:	gap of unknown length	gap	29535..29634
* 21677	24623:	contig of 2947 bp in length	gap	/estimated_length=unknown
* 24624	24723:	gap of unknown length	gap	32649..32748
* 24724	28116:	contig of 3393 bp in length	gap	/estimated_length=unknown
* 28117	28216:	gap of unknown length	gap	40513..40612
* 28217	29534:	contig of 1318 bp in length	gap	/estimated_length=unknown
* 29535	29634:	gap of unknown length	gap	43862..43961
* 29635	32648:	contig of 3014 bp in length	gap	/estimated_length=unknown
* 32649	32748:	gap of unknown length	gap	48430..48529
* 32749	40512:	contig of 7764 bp in length	gap	/estimated_length=unknown
* 40513	40612:	gap of unknown length	gap	59230..59329
* 40613	43861:	contig of 3249 bp in length	gap	/estimated_length=unknown
* 43862	43961:	gap of unknown length	gap	60890..60989
* 43962	48429:	contig of 4468 bp in length	gap	/estimated_length=unknown
* 48430	48529:	gap of unknown length	gap	65148..65247
* 48530	59229:	contig of 10700 bp in length	gap	/estimated_length=unknown
* 59230	59329:	gap of unknown length	gap	67581..67680
* 59330	60889:	contig of 1560 bp in length	gap	/estimated_length=unknown
* 60890	60989:	gap of unknown length	gap	68777..68876
* 60990	65147:	contig of 4158 bp in length	gap	/estimated_length=unknown
* 65148	65247:	gap of unknown length	gap	85494..85593
* 65248	67580:	contig of 2333 bp in length	gap	/estimated_length=unknown
* 67581	67680:	gap of unknown length	gap	90518..90617
* 67681	68776:	contig of 1096 bp in length	gap	/estimated_length=unknown
* 68777	68876:	gap of unknown length	gap	111501..111600
* 68877	85493:	contig of 16617 bp in length	gap	/estimated_length=unknown
* 85494	85593:	gap of unknown length	gap	112665..112764
* 85594	90517:	contig of 4924 bp in length	gap	/estimated_length=unknown
* 90518	90617:	gap of unknown length	gap	122910..123009
* 90618	111500:	contig of 20883 bp in length	gap	/estimated_length=unknown
* 111501	111600:	gap of unknown length	gap	127131..127230
* 111601	112664:	contig of 1064 bp in length	gap	/estimated_length=unknown
* 112665	112764:	gap of unknown length	gap	130720..130819
* 112765	122909:	contig of 10145 bp in length	gap	/estimated_length=unknown
* 122910	123009:	gap of unknown length	gap	140094..140193
* 123010	127130:	contig of 4121 bp in length	gap	/estimated_length=unknown
* 127131	127230:	gap of unknown length	gap	162844..162943
* 127231	130719:	contig of 3489 bp in length	gap	/estimated_length=unknown
* 130720	130819:	gap of unknown length	gap	167187..167286
* 130820	140093:	contig of 9274 bp in length	gap	/estimated_length=unknown
* 140094	140193:	gap of unknown length	gap	169931..170030
* 140194	162843:	contig of 22650 bp in length	gap	/estimated_length=unknown
* 162844	162943:	gap of unknown length	gap	175432..175531
* 162944	167186:	contig of 4243 bp in length	gap	/estimated_length=unknown
* 167187	167286:	gap of unknown length	gap	177306..177405
* 167287	169300:	contig of 2644 bp in length	gap	/estimated_length=unknown
* 169301	170030:	gap of unknown length	gap	178664..178763
* 170031	175431:	contig of 5401 bp in length	gap	/estimated_length=unknown
* 175432	175531:	gap of unknown length	gap	
* 175532	177305:	contig of 1774 bp in length	gap	
* 177306	177405:	gap of unknown length	gap	
* 177406	178663:	contig of 1258 bp in length	gap	
* 178664	178763:	gap of unknown length	gap	
* 178764	182004:	contig of 3241 bp in length.	gap	
Location/Qualifiers				
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/organism="Zea mays"				
/mol_type="genomic DNA"				
/strain="B73"				
/db_xref="taxon:4577"				
/clone="ZMWBBC0261N01"				
2005..2104				
/estimated_length=unknown				
15141..15240				
/estimated_length=unknown				
16542..16641				
/estimated_length=unknown				
21577..21676				
/estimated_length=unknown				
24624..24723				
/estimated_length=unknown				
28117..28216				
FEATURES				
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gap	7947.8046	/estimated_length=unknown	
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gap	23006.23105	/estimated_length=unknown	
gap	31192.31291	/estimated_length=unknown	
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gap	45341.45440	/estimated_length=unknown	
gap	50240.50339	/estimated_length=unknown	
gap	55709.55808	/estimated_length=unknown	
gap	66591.66690	/estimated_length=unknown	
gap	74476.74575	/estimated_length=unknown	
gap	84290.84389	/estimated_length=unknown	
gap	86687.86786	/estimated_length=unknown	
gap	89394.89493	/estimated_length=unknown	
gap	99396.99495	/estimated_length=unknown	
gap	104791.104890	/estimated_length=unknown	
gap	108665.108764	/estimated_length=unknown	
gap	111926.112025	/estimated_length=unknown	
gap	115968.116067	/estimated_length=unknown	
gap	117224.117323	/estimated_length=unknown	
gap	118464.118563	/estimated_length=unknown	
gap	120859.120958	/estimated_length=unknown	
gap	125844.125943	/estimated_length=unknown	
gap	129477.129576	/estimated_length=unknown	
gap	134150.134249	/estimated_length=unknown	
gap	143177.143276	/estimated_length=unknown	
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gap	155362.155461	/estimated_length=unknown	
gap	158246.158345	/estimated_length=unknown	
gap	159779.159878	/estimated_length=unknown	
gap	173402.173501	/estimated_length=unknown	
gap	175779.175878	/estimated_length=unknown	
gap	179686.179785	/estimated_length=unknown	
ORIGIN			
Query Match			7.4%; Score 61; DB 14; Length 193326;
Best Local Similarity			100.0%; Pred. No. 8.8e-25;
Matches			61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	143	CGAATATAGAGCTAGACACTGTGCTTCGTCACAGATACATGCTCTTGAGATTTTACAT	202
Db	192227	CGAATATAGAGCTAGACACTGTGCTTCGTCACAGATACATGCTCTTGAGATTTTACAT	192286

QY

203 T 203

Db

192287 T 192287

RESULT 7

AC155517/c

LOCUS

DEFINITION

AC155517

AC155517.2 GI:58082377

HTG; HTGS_PHASE1

Zeasays

Zeasays

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AC155517

148120 bp

DNA

linear

HTG 25-JAN-2005

Zeasays strain B73 clone ZMWBc0062P13, *** SEQUENCING IN PROGRESS

***, 15 unordered pieces.

AC155517

AC155517.2 GI:58082377

HTG; HTGS_PHASE1

Zeasays

Zeasays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 148120)

Chan,A.P., Pertea,G., Zheng,L., Cheung,F., Lee,D., Koo,H., Utterback,T.R., Feldblyum,T.V., Rabinowicz,P., Fraser,C.M., Schubert,K., SanMiguel,P., Ma,J., Pontaroli,A.C., Rohlfing,T., Budiman,A., Bedell,J.A., Lakey,N., Barbazuk,B., Bennetzen,J. and Quackenbush,J.

Consortium for Maize Genomics - BAC skim sequencing and assembly

Unpublished

2 (bases 1 to 148120)

Chan,A.P., Pertea,G., Zheng,L., Cheung,F., Lee,D., Koo,H., Utterback,T.R., Feldblyum,T.V., Rabinowicz,P., Fraser,C.M., Schubert,K., SanMiguel,P., Ma,J., Pontaroli,A.C., Rohlfing,T., Budiman,A., Bedell,J.A., Lakey,N., Barbazuk,B., Bennetzen,J. and Quackenbush,J.

Direct Submission

Submitted (15-JAN-2005) The Institute for Genomic Research (TIGR), 9712 Medical Center Dr, Rockville, MD 20850

3 (bases 1 to 148120)

Chan,A.P., Pertea,G., Zheng,L., Cheung,F., Lee,D., Koo,H., Utterback,T.R., Feldblyum,T.V., Rabinowicz,P., Fraser,C.M., Schubert,K., SanMiguel,P., Ma,J., Pontaroli,A.C., Rohlfing,T., Budiman,A., Bedell,J.A., Lakey,N., Barbazuk,B., Bennetzen,J. and Quackenbush,J.

Direct Submission

Submitted (25-JAN-2005) The Institute for Genomic Research (TIGR), 9712 Medical Center Dr, Rockville, MD 20850

On Jan 25, 2005 this sequence version replaced gi:57863038.

----- Trace submission

Center name: TIGR

Seq lib id: ZOBH

----- Project informaton

Web site: <http://www.tigr.org/tdb/tgi/maize/>

Contact: maize@tigr.org

* NOTE: This is a 'working draft' sequence. It currently

* consists of 15 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.

* 1

* 7711: contig of 7711 bp in length

* 7812: gap of unknown length

* 7815: contig of 30354 bp in length

* 38166: gap of unknown length

* 38265: contig of 1983 bp in length

* 40248: gap of unknown length

* 40348: contig of 15404 bp in length

* 55752: gap of unknown length

* 55853: contig of 5841 bp in length

* 55753: gap of unknown length

* 55853: contig of 5841 bp in length

* 61694: gap of unknown length

* 61793: contig of 18109 bp in length

* 61794: gap of unknown length

* 79903: gap of unknown length

* 80002: gap of unknown length

Sciences West, 448A, P.O. Box 210088, University of Arizona,
Tucson, AZ 85721, USA (<http://www.genome.arizona.edu>)
----- Project Information
Center Project name: L30352
Center clone name: 496_L_17

* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor

* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 1 62677: contig of 62677 bp in length
* 62678 112468: gap of unknown length
* 62778 112468: contig of 49691 bp in length.

FEATURES

Location/Qualifiers
1..112468
/organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"
/clone="ZMWBBC0496L17"
/clone_lib="CHORI-201 Maize B73 BAC MhoI Library"
62678..62777
/estimated_length=unknown

ORIGIN

Query Match 5.6%; Score 46; DB 14; Length 112468;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGCAGGCTACTCCAGTATAGACACACGCTAAACACACATAT 46

Db 2368 CTGCAGGCTACTCCAGTATAGACACACGCTAAACACACATAT 2413

RESULT 9
AC149827/c
LOCUS AC149827 143793 bp DNA linear HTG 03-FEB-2005
DEFINITION Zea mays clone ZMWBBC0051H21, *** SEQUENCING IN PROGRESS ***, 8
unordered pieces.

AC149827
AC149827.2 GI:57790148
HTG: HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEPIN.

SOURCE

Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 143793)
Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bhatti, A.K.

and Messing, J.

Zea mays, clone ZMWBBC0051H21

Unpublished

2 (bases 1 to 143793)

Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bhatti, A.K.,
Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S.,
Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L.,
Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., Corum, B., DeArelano, K., Diaz, J.S., Dodge, S.,
Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P.,
Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L.,
Grand-pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J.,
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P.,
Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,

Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C.,
Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,
Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (22-JUN-2004) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 143793)

Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bhatti, A.K.,
Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S.,
Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L.,
Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., Corum, B., DeArelano, K., Diaz, J.S., Dodge, S.,
Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P.,
Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L.,
Grand-pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J.,
Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
Liu, G., Liu, X., Lui, A., Mabbitt, R., Maclean, C., Macdonald, P.,
Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C.,
Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,
Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (03-FEB-2005) Broad Institute of MIT and Harvard, 320
Charles Street, Cambridge, MA 02141, USA

On Jan 14, 2005 this sequence version replaced gi:49035053.

All repeats were identified using RepeatMasker:

Smith, A.F.A. & Green, P. (1996-1997)

<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center

Center: Broad Institute of MIT and Harvard

Center code: W1BR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@broad.mit.edu

Bhatti, AK and Messing, J: The Plant Genome Initiative at
Rutgers, Waksman Institute, Rutgers, The State University of New
Jersey, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA
(<http://pgir.rutgers.edu>)
Butler, E and Wing, R: Arizona Genomics Institute, Biological
Sciences West, 448A, P.O. Box 210088, University of Arizona,
Tucson, AZ 85721, USA (<http://www.genome.arizona.edu>)

----- Project Information

Center project name: L30279

Center clone name: 51_H_21

* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

* 1 30907: contig of 30907 bp in length
* 30908 3007: gap of unknown length
* 31008 36273: contig of 5266 bp in length
* 36274 36373: gap of unknown length
* 36374 45582: contig of 9209 bp in length
* 45583 45682: gap of unknown length
* 45683 78484: contig of 32802 bp in length
* 78485 78584: gap of unknown length
* 78585 97556: contig of 21172 bp in length
* 97557 99857: gap of unknown length
* 99857 120940: contig of 21084 bp in length

* 120941 121040: gap of unknown length
 * 121041 123150: contig of 2110 bp in length
 * 123151 123250: gap of unknown length
 * 123251 143793: contig of 20543 bp in length.

FEATURES

source

Location/Qualifiers
 1. 143793
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /db_xref="taxon:4577"
 /clone_lib="CHORI-201 Maize B73 BAC EcoRI Library"
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 /estimated_length=unknown
 36274..36373
 /estimated_length=unknown
 45583..45582
 /estimated_length=unknown
 78485..78584
 /estimated_length=unknown
 99757..99856
 /estimated_length=unknown
 120941..121040
 /estimated_length=unknown
 123151..123250
 /estimated_length=unknown

ORIGIN

Query Match 5.6%; Score 46; DB 14; Length 143793;
 Best Local Similarity 100.0%; Pred. No. 1.4e-15;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGACGGTACTCCAGTATAGACACAGCTAAACACACATAT 46
 Db 29159 CTGACGGTACTCCAGTATAGACACAGCTAAACACACATAT 29114

RESULT 10
 AC166637/c
 LOCUS AC166637 132900 bp DNA linear HTG 03-AUG-2005
 DEFINITION Zea mays strain B73 clone ZMWBb0171P15, *** SEQUENCING IN PROGRESS
 ACCSSION AC166637
 VERSION AC166637.1 GI:71725485
 KEYWORDS HTG; HTGS_PHASE1.
 SOURCE Zea mays
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 132900)
 Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
 Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
 Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlffing, T.,
 Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
 Quackenbush, J.
 Consortium for Maize Genomics - BAC skim sequencing and assembly
 Unpublished
 2 (bases 1 to 132900)
 Chan, A.P., Pertea, G., Zheng, L., Cheung, F., Lee, D., Koo, H.,
 Utterback, T.R., Feldblyum, T.V., Rabinowicz, P., Fraser, C.M.,
 Schubert, K., SanMiguel, P., Ma, J., Pontaroli, A.C., Rohlffing, T.,
 Budiman, A., Bedell, J.A., Lakey, N., Barbazuk, B., Bennetzen, J. and
 Quackenbush, J.
 Consortium for Maize Genomics - BAC skim sequencing and assembly
 Unpublished

TITLE
 JOURNAL
 REFERENCE

Submitted (03-AUG-2005) The Institute for Genomic Research (TIGR),
 9712 Medical Center Dr, Rockville, MD 20850
 COMMENT
 Center name: TIGR
 Seq_id: ZOED
 Project information
 Web site: <http://www.tigr.org/tdb/tgi/maize/>
 Contact: maize@tigr.org

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 3 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved

* 1 35920: contig of 35920 bp in length
 * 35921 36020: gap of unknown length
 * 36021 80081: contig of 44061 bp in length
 * 80082 80181: gap of unknown length
 * 80182 132900: contig of 52719 bp in length.

FEATURES

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Location/Qualifiers
 1. 132900
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="taxon:4577"
 /clone="ZMWBb0171P15"
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 /estimated_length=unknown
 80082..80181
 /estimated_length=unknown

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 6.9e-12;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 102 ATTCATAAATAAGTGACCAATCAGATAGTCTCCTGTC 141
 Db 57921 ATTCATAAATAAGTGACCAATCAGATAGTCTCCTGTC 57882

RESULT 11

ZMPRO2MR 830 bp mRNA linear PLN 18-APR-2005
 LOCUS Z.mays ZmPRO2 mRNA for profilin 2.
 DEFINITION X73280
 ACCESSION X73280.1 GI:313139
 VERSION
 KEYWORDS profilin.
 SOURCE Zea mays
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1
 Staiger, C.J., Goodbody, K.C., Hussey, P.J., Valenta, R., Drobak, B.K.
 and Lloyd, C.W.
 The profilin multigene family of maize: differential expression of
 three isoforms
 Plant J. 4 (4), 631-641 (1993)
 8252067
 2 (bases 1 to 830)
 Staiger, C.J.
 Direct Submission
 Submitted (09-JUN-1993) C.J. Staiger, John Innes Centre for Plant
 Science Res., Dept. of Cell Biology, Colney Lane, Norwich NR4 7UH,
 UK

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 PUBMED
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

Location/Qualifiers
 1. 830
 /organism="Zea mays"
 /mol_type="mRNA"
 /strain="inbred A188"
 /db_xref="taxon:4577"
 /cell_type="pollen"
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 /product="profilin 2"
 /protein_id="CAA51719.1"
 /db_xref="GI:313140"
 /db_xref="GOA:P35082"

FEATURES

source

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/db_xref="UniProt/Swiss-Prot:P35082"
 /translation="MSDRKMSWQAYVDEHLMCEIEGHLAAALVGHGDAWAQSTA
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 93.95
 /note="2nd start codon; in-frame"

misc_feature

ORIGIN

Query Match 4.6%; Score 38; DB 15; Length 830;
 Best Local Similarity 100.0%; Pred. No. 8.5e-11;
 Matches: 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 786 CCTCTCCCTCCCTCCGATCCATCTTCAGCGCAG 823

DB 27 CCTCTCCCTCCCTCCGATCCATCTTCAGCGCAG 64

RESULT 12
 AC145389 198102 bp DNA linear HTG 20-JUN-2004
 LOCUS Zea mays clone ZMMBc0054A01, *** SEQUENCING IN PROGRESS ***, 4
 DEFINITION ordered pieces.
 ACCESSION AC145389
 VERSION AC145389.6 GI:48762556
 KEYWORDS HTG; HTGS_PHASE2; HTGS_FULLTOP; HTGS_ACTIVEFIN.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 198102)
 Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K.
 and Messing, J.

Zeas mays, clone ZMMBc0054A01

2 (bases 1 to 198102)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
 Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
 Boguslavsky, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,
 Collumore, A., Cook, A., Cooke, P., Corum, B., DeArelano, K.,
 Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
 Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S.,
 Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,
 Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
 Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
 Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., MacLean, C.,
 Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,
 Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,
 Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
 O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
 Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
 Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C.,
 Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
 Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M.,
 Vasiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
 Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (01-JUL-2003) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 198102)
 Birren, B., Nusbaum, C., Lander, E., Butler, E., Wing, R., Bharti, A.K.,
 Messing, J., Abouelleil, A., Allen, N., Anderson, M., Anderson, S.,
 Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
 Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collumore, A.,
 Cook, A., Cooke, P., Corum, B., DeArelano, K., Diaz, J.S., Dodge, S.,
 Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P.,
 Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L.,
 Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J.,
 Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A.,
 Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K.,
 Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P.,
 Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J.,
 Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,

Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
 O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
 Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
 Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C.,
 Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
 Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M.,
 Vasiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
 Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (20-JUN-2004) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Jun 16, 2004 this sequence version replaced gi:4817652.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@broad.mit.edu

Bharti, AK and Messing, J.: The Plant Genome Initiative at
 Rutgers, Waksman Institute, Rutgers, The State University of New
 Jersey, 190 Frelinghuysen Road, Piscataway, NJ 08854, USA
 (http://pgir.rutgers.edu)

Butler, E and Wing, R.: Arizona Genomics Institute, Biological
 Sciences West, 448A, P.O. Box 210088, University of Arizona,
 Tucson, AZ 85721, USA (http://www.genome.arizona.edu)

----- Project Information

Center project name: L29613

Center clone name: 54_A1

----- Consensus Information

This consensus is derived from a shotgun assembly that has been
 manually curated. It is the best representation of the BAC that we
 can generate without further laboratory work. The draft assembly
 has been edited, and if possible, ends identified by vector as well
 as by BAC end sequences, and contigs ordered and oriented. Bases
 that are not Ns are either above Q20 or manually edited. This
 assembly was performed with Phrap. All trace files for this project
 are available at the NCBI trace repository
 (http://www.ncbi.nlm.nih.gov/Traces/trace.cgi?). An exact list of
 reads used in this assembly are available at
 http://www.broad.mit.edu/annotation/plants/maize/randomclones.html.

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 4 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * been provided by the submitter.

* This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 20266: contig of 20266 bp in length
 * 20267 20366: gap of 100 bp
 * 20367 78634: contig of 58268 bp in length
 * 78635 78734: gap of 100 bp
 * 78735 140318: contig of 61584 bp in length
 * 140319 140418: gap of 100 bp
 * 140419 198102: contig of 57684 bp in length.

FEATURES

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1. 198102
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 /mol_type="genomic DNA"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /clone="ZMMBc0054A01"
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 20267 - 20366
 /estimated_length=100
 78635 - 78734
 /estimated_length=100
 140319 - 140418

gap

gap

gap

COMMENT On Jan 14, 2005 this sequence version replaced gi:49035040.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Broad Institute of MIT and Harvard
Center code: W1BR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@broad.mit.edu

Bharti, AK and Messing, J: The Plant Genome Initiative at
Rutgers, Waksman Institute, Rutgers, The State University of New
Jersey, 150 Frelinghuysen Road, Piscataway, NJ 08854, USA
(http://pgir.rutgers.edu)
Butler, E and Wing, R: Arizona Genomics Institute, Biological
Sciences West, 448A, P.O. Box 210088, University of Arizona,
Tucson, AZ 85721, USA (http://www.genome.arizona.edu)
----- Project Information
Center project name: L30238
Center clone name: 309_E_13

* NOTE: This is a 'working draft' sequence. It currently
* consists of 7 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 2922: contig of 2922 bp in length
* 2923 3022: gap of unknown length
* 3023 15817: contig of 12795 bp in length
* 15818 15917: gap of unknown length
* 15918 25218: contig of 9301 bp in length
* 25219 25318: gap of unknown length
* 25319 42542: contig of 17224 bp in length
* 42543 42642: gap of unknown length
* 42643 45994: contig of 3352 bp in length
* 45995 46094: gap of unknown length
* 46095 68616: contig of 22522 bp in length
* 68617 68716: gap of unknown length
* 68717 69497: contig of 781 bp in length.
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/clone_lib="ZMWBB0309E13"
/clone_lib="CUGI. Maize B73 BAC HindIII Library"
2923..3022
/estimated_length=unknown
gap
15818..15917
/estimated_length=unknown
gap
25219..25318
/estimated_length=unknown
gap
42543..42642
/estimated_length=unknown
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45995..46094
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Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 207 CCCCTAGACACACTTAAAGACACACACTTAAAGACAC 242
DB 32782 CCCCTAGACACACTTAAAGACACACACTTAAAGACAC 32747

AF348367/c
LOCUS AF348367 1257 bp DNA linear PLN 02-MAR-2002
DEFINITION Zea mays inbred B77 beta-keto acyl reductase gene, partial cds.
ACCESSION AF348367
VERSION AF348367.1 GI:19070512
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1257)
AUTHORS Dietrich, C.R., Cui, F., Packila, M.L., Li, J., Ashlock, D.A.,
Nikolau, B.J. and Schnable, P.S.
TITLE Maize Mu transposons are targeted to the 5' untranslated region of
the g18 gene and sequences flanking Mu target-site duplications
exhibit nonrandom nucleotide composition throughout the genome
Genetics 160 (2), 697-716 (2002)
JOURNAL 11861572
PUBMED 11861572
REFERENCE 2 (bases 1 to 1257)
AUTHORS Dietrich, C.R., Packila, M.L., Li, J., Ashlock, D.A., Nikolau, B.J. and
Schnable, P.S.
TITLE Direct Submission
JOURNAL Submitted (12-FEB-2001) Zoology and Genetics, Iowa State
University, B420 Agronomy Hall, Ames, IA 50011, USA
FEATURES
Location/Qualifiers
1..1257
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="inbred B77"
/db_xref="taxon:4577"
<946..>1257
/product="beta-keto acyl reductase"
946..>1257
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/product="beta-keto acyl reductase"
/protein_id="AAU83898.1"
/db_xref="GI:19070513"
/translation="MAGTCAHVSFLRAQPAWALAAVGLLVAVRAAARFALVWVAAF
LRPGKPLRRRYGAWVVTGATDGIQRAVAFRLAASGLGLVLRNQEKLAAVAEIK
RH"
ORIGIN
Query Match 4.3%; Score 35; DB 15; Length 1257;
Best Local Similarity 100.0%; Pred. No. 6.1e-09;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 324 ATTCAATAAATTAAAGTGACCAATCAGATAGTCTC 290
Search completed: March 5, 2006, 12:38:18
Job time : 4265 secs